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OLFACTORY RECEPTOR GENES AND PSEUDOGENES IN PRIMATES AND MOUSE

The present invention relates to the discovery of olfactory receptor genes and pseudogenes in primates and mouse, the olfactory receptors encoded by these genes and their utilization.

Mammals are able to discriminate between thousands of odour molecules. This capacity relies on a multigene family encoding 500 - 1000 olfactory receptors (OR) (1). These receptors are expressed mainly in the olfactory epithelium and have been found in a number of species including mammals (1-5), birds (6, 7), amphibians (8) and fish (9). All these receptors belong to the G protein-coupled receptor (GPCR) superfamily and share features of sequence and structure, such · as seven hydrophobic transmembrane domains (7TM).

The sense of smell plays an important role in mammalian social behavior, location of food and detection of predators. However, mammals vary in their olfactory ability (10, 11). The sense of smell in primates is greatly reduced (microsmatic) with respect to other mammals such as dogs (12) or rodents (10, 11). Various explanations for the differences in olfactory performance have been hypothesized. Differences in the anatomical structures (size, location) devoted to olfaction could partly explain these differences. For example, dogs, which have an olfactory sensitivity up to 100 times greater than humans, have on average $\sim 100 \text{ cm}^2$ of olfactory epithelium whilst humans have only 10 cm^2 ((4) and references therein). Variations in the size and diversity of the expressed OR gene family could also account for these differences. The Applicant recently demonstrated that the human OR gene repertoire is distributed in over 25 chromosomal sites, and over 70% of these OR genes are pseudogenes, i.e. the sequences have accumulated deleterious mutations such as in-frame stop codons and/or frameshifts (3). This finding 'led us to hypothesize that the reduction of the sense of smell observed in primates could parallel the reduction of the number of functional OR genes.

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In order to test this hypothesis the Applicant wished to characterize the evolution of the OR gene family in other primates. A random survey of OR genes from primate hominoids to prosimians was performed. In parallel, a mouse OR-enriched library from genomic DNA in order to sequence a number of OR was constructed. The comparison of the OR gene repertoire from macrosmatic mouse and primates provides insight into the evolution of this multigene family and could reflect the evolution of a sensory function in mammals in response to selective constraints.

of concerns a molecule invention thus nucleic acid constituted by or comprising a sequence chosen among those represented in the list of sequences in the 15 appendix under the numbers SEQ ID No. 3, SEQ ID No. 12, ID No. 21, SEQ ID No. 22, SEQ ID No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ 20 ID No. 43, SEQ ID No. 52, SEQ ID No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID No. 60, SEQ ID No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 25 120, SEQ ID No. 121, SEQ ID No. 122, SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEQ ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 233, SEQ ID No. 238, SEQ ID 30 No. 239, SEQ ID No. 244, SEQ ID No. 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEQ ID No. 317, SEQ ID No. 324, SEQ ID No. 327, SEQ ID No. 350, SEQ ID No. 363, SEQ 35 ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID

No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ 5 ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, 10 SEQ ID No. 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEQ ID No. 180, SEQ ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 15 193, SEQ ID No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID 20 No. 242, SEQ ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266, SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ 25 ID No. 289, SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330, 30 SEQ ID No. 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ ID No. 355, SEQ ID No. 357, SEQ ID No. 359, SEQ ID No. 361, SEQ ID No. 364, SEQ ID No. 366, SEQ ID No. 368, SEQ ID No. 35 370, SEQ ID No. 372, SEQ ID No. 374, SEQ ID No. 376, SEQ ID No. 378, SEQ ID No. 380, SEQ ID No. 382, SEQ ID No. 384, SEQ ID No. 386, SEQ ID No. 388, SEQ ID No. 390, SEQ ID No. 392, SEQ ID No. 394, SEQ ID No. 396, SEQ ID No. 398, SEQ ID No.

400, SEQ ID No. 402, SEQ ID No. 404, SEQ ID No. 406, SEQ ID No. 408, SEQ ID No. 410, SEQ ID No. 412, SEQ ID No. 414, SEQ ID No. 416, SEQ ID No. 418, SEQ ID No. 420, SEQ ID No. 422, SEQ ID No. 424, SEQ ID No. 426, SEQ ID No. 428 and SEQ ID No. 430.

The invention relates more particularly to molecule of nucleic acid comprising or constituted of an encoding nucleic sequence for an olfactory receptor or for a fragment of an olfactory receptor. In the appendix, the encoding nucleic sequences for an olfactory receptor or for 10 a fragment of an olfactory receptor are the sequences chosen among those represented in the list of sequences in the appendix under the numbers SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID 15 No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID 20 No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID 25 No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEQ ID No. 180, SEQ 30 ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 193, SEQ ID No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, 35 SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID No. 242, SEQ ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266,

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SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ ID No. 289, SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 5 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330, SEQ ID No. 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID 10 No. 351, SEQ ID No. 353, SEQ ID No. 355, SEQ ID No. 357, SEQ ID No. 359, SEQ ID No. 361, SEQ ID No. 364, SEQ ID No. 366, SEQ ID No. 368, SEQ ID No. 370, SEQ ID No. 372, SEQ ID No. 374, SEQ ID No. 376, SEQ ID No. 378, SEQ ID No. 380, SEQ ID No. 382, SEQ ID No. 384, SEQ ID No. 386, SEQ ID No. 388, SEQ 15 ID No. 390, SEQ ID No. 392, SEQ ID No. 394, SEQ ID No. 396, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 402, SEQ ID No. 404, SEQ ID No. 406, SEQ ID No. 408, SEQ ID No. 410, SEQ ID No. 412, SEQ ID No. 414, SEQ ID No. 416, SEQ ID No. 418, SEQ ID No. 420, SEO ID No. 422, SEQ ID No. 424, SEQ ID No. 426, 20 SEQ ID No. 428, SEQ ID No. 430. Evidently the invention also concerns the nucleotide sequences derived from the above sequences, for example from the degeneracy of the genetic for the proteins presenting and which encodes characteristics and properties of olfactory receptors. 25 encoding nucleic sequences for an olfactory receptor or for a fragment of an olfactory receptor are different from the pseudogenes presented in this invention. The pseudogenes correspond to the sequences in the appendix under the numbers SEQ ID No. 3, SEQ ID No. 12, SEQ ID No. 21, SEQ ID 30 No. 22, SEQ ID No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 52, SEQ ID No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID 35 No. 60, SEQ ID No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 120, SEQ ID No. 121,

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SEQ ID No. 122, SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEQ ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 233, SEQ ID No. 238, SEQ ID No. 239, SEQ ID No. 244, SEQ ID No. 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEQ ID No. 317, SEQ ID No. 324, SEQ ID No. 327, SEQ ID No. 350 and SEQ ID No. 363.

invention also concerns a molecule The nucleic sequence which encode for the olfactory receptors or fragments of olfactory receptors whose amino acid sequences are represented in the list of sequences in the appendix under the numbers SEQ ID No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137, SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No. 146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ ID No. 164, SEQ ID No. 166, SEQ ID No. 168, SEQ ID No. 170, SEQ ID No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No. 179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204, SEQ ID No. 209, SEQ ID No. 211, SEQ ID No. 214, SEQ ID No. 218, SEQ ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248, SEQ ID No. 250, SEQ ID No. 253, SEQ ID No. 255, SEQ ID No. 257, SEQ ID No. 263, SEQ

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ID No. 265, SEQ ID No. 267, SEQ ID No. 269, SEQ ID No. 271, SEQ ID No. 274, SEQ ID No. 276, SEQ ID No. SEQ ID No. 278, SEO ID No. 281, SEQ ID No. 284, SEQ ID No. 286, SEQ ID No. 288, SEQ ID No. 290, SEQ ID No. 294, 296, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 302, SEQ ID No. 304, SEQ ID No. 306, SEQ ID No. 308, SEQ ID No. 310, SEQ ID No. 312, SEQ ID No. 316, SEQ ID No. 319, SEQ ID No. 321, SEQ ID No. 323, SEQ ID No. 326, SEQ ID No. 329, SEQ ID No. 331, SEQ ID No. 333, SEQ ID No. 335, SEQ ID No. 337, SEQ ID No. 339, SEQ ID No. 341, SEQ ID No. 343, SEQ ID No. 345, SEQ ID No. 347, SEQ ID No. 349, SEQ ID No. 352, SEQ ID No. 354, SEQ ID No. 356, SEQ ID No. 358, SEQ ID No. 360, SEQ ID No. 362, SEQ ID No. 365, SEQ ID No. 367, SEQ ID No. 369, SEQ ID No. 371, SEQ ID No. 373, SEQ ID No. 375, SEQ ID No. 377, SEQ ID No. 379, SEQ ID No. 381, SEQ ID No. 383, SEQ ID No. 385, SEQ ID No. 387, SEQ ID No. 389, SEQ ID No. 391, SEQ ID No. 393, SEQ ID No. 395, SEQ ID No. 397, SEQ ID No. 399, SEQ ID No. 401, SEQ ID No. 403, SEQ ID No. 405, SEQ ID No. 407, SEQ ID No. 409, SEQ ID No. 411, SEQ ID No. 413, SEQ ID No. 415, SEQ ID No. 417, SEQ ID No. 419, SEQ ID No. 421, SEQ ID No. 423, SEQ ID No. 425, SEQ ID No. 427, SEQ ID No. 429 and SEQ ID No. 431.

The invention thus concerns more particularly a purified olfactory receptor constituted by or comprising the sequence of amino acids chosen among those represented in the list of amino acid sequences under the numbers SEQ ID No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137, SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No. 146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ

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ID No. 164, SEQ ID No. 166, SEQ ID No. 168, SEQ ID No. 170, SEQ ID No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No. 179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204, SEO ID No. 209, SEQ ID No. 211, SEQ ID No. 214, SEQ ID No. 218, SEQ ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248, SEO ID No. 250, SEO ID No. 253, SEQ ID No. 255, SEQ ID No. 257, SEQ ID No. 263, SEQ ID No. 265, SEQ ID No. 267, SEQ ID No. 269, SEQ ID No. 271, SEQ ID No. 274, SEQ ID No. 276, SEQ ID No. SEQ ID No. 278, SEQ ID No. 281, SEQ ID No. 284, SEQ ID No. 286, SEQ ID No. 288, SEQ ID No. 290, SEQ ID No. 294, 296, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 302, SEQ ID No. 304, SEO ID No. 306, SEQ ID No. 308, SEQ ID No. 310, SEQ ID No. 312, SEQ ID No. 316, SEQ ID No. 319, SEQ ID No. 321, SEQ ID No. 323, SEQ ID No. 326, SEQ ID No. 329, SEQ ID No. 331, SEQ ID No. 333, SEQ ID No. 335, SEQ ID No. 337, SEQ ID No. 339, SEQ ID No. 341, SEQ ID No. 343, SEQ ID No. 345, SEQ ID No. 347, SEQ ID No. 349, SEQ ID No. 352, SEQ ID No. 354, SEQ ID No. 356, SEQ ID No. 358, SEQ ID No. 360, SEQ ID No. 362, SEQ ID No. 365, SEQ ID No. 367, SEQ ID No. 369, SEQ ID No. 371, SEQ ID No. 373, SEQ ID No. 375, SEQ ID No. 377, SEQ ID No. 379, SEQ ID No. 381, SEQ ID No. 383, SEQ ID No. 385, SEO ID No. 387, SEQ ID No. 389, SEQ ID No. 391, SEQ ID No. 393, SEQ ID No. 395, SEQ ID No. 397, SEQ ID No. 399, SEQ ID No. 401, SEQ ID No. 403, SEQ ID No. 405, SEQ ID No. 407, SEQ ID No. 409, SEQ ID No. 411, SEQ ID No. 413, SEQ ID No. 415, SEQ ID No. 417, SEQ ID No. 419, SEQ ID No. 421, SEQ ID No. 423, SEQ ID No. 425, SEQ ID No. 427, SEQ ID No. 429 and SEQ ID No. 431.

Another aim of the invention is polyclonal or monoclonal antibodies directed against at least one receptor of the invention, a derivative or a fragment of these. These antibodies can be prepared by the methods described in the literature. According to prior art techniques, polyclonal antibodies are formed by the injection of proteins, extracted from the epithelium or produced by genetic

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animals, and then transformation of a host, into and antibodies from the recuperation of antiserums antiserums for example by affinity chromatography. The monoclonal antibodies can be produced by fusing myeloma cells with spleen cells from animals previously immunised using the receptors of the invention. These antibodies are useful in the search for new olfactory receptors or the homologues of these receptors in other mammals or again for studying the relationship between the receptors of different individuals or species.

The invention also concerns a vector comprising at least one molecule of nucleic acid above, advantageously associated with adapted control sequences, together with a production or expression process in a cellular host of a receptor of the invention or a fragment thereof. The preparation of these vectors as well as the production or expression in a protein host of the invention can be carried out by molecular biology and genetic engineering techniques well known to the professional.

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A molecule of encoding nucleic acid for an olfactory receptor or a vector according to the invention can also be used to transform animals and establish a line of transgenic animals.

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The vector used is chosen in function of the host into which it is to be transferred; it can be any vector such as a plasmid.

Thus the invention also relates to cellular hosts expressing olfactory receptors obtained in conformity with the preceding processes.

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The invention also relates to nucleic and oligonucleotide probes prepared from the molecules of nucleic acid according to the invention.

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These probes, marked advantageously, are useful for hybridisation detection of similar receptor sequences in other individuals or species. According to prior art techniques, these probes are put into contact with a biological sample. Different hybridisation techniques can be

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used, such as Dot-blot hybridisation or replica hybridisation (Southern technique) or other techniques (DNA chips). Such probes constitute the tools making it possible to detect similar sequences quickly in the encoding genes

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for olfactory receptors which allow study of the presence, origin and preservation of these proteins.

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The oligonucleotides are useful for PCR experiments, for example to search for genes in other species or with a diagnostic aim.

The olfactory receptors are proteins with 7 transmembranous domains coupled with G proteins. Attachment of a ligand to a receptor brings about a change in the conformation of the receptor, and inside the cell, and this signal is transducted through the intermediary of second messengers. Consequently, the aim of the invention is a screening process for compounds capable of constituting ligands of the receptors described above consisting of putting in contact one compound and one or several of said receptors and of measuring by any appropriate means the affinity between said compound and said receptor.

The contact between the compound to be tested and the olfactory receptor or receptors of the invention can be carried out by using the hosts described above and expressing said receptors at least at their surface. It can consist of a line of immortalised cells, olfactory or not, transfected by a vector carrying cDNA making it possible to express at its surface and at a high level a functional recombinant olfactory receptor. If the compound tested constitutes a ligand, its contact with the transformed cells, induces intracellular signals which result from the fixation of said compound on the receptor.

The contact of the compounds to be tested with the receptors of the invention can also be carried out by fixing one or several receptors on one or several membranes. The olfactory receptors of the invention can thus also be integrated with a bio-sensor. In such a system, it is possible to visualise in real time the interactions between the compound being tested and the receptor. One of the

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partners of the couple receptor/ligand is fixed on an interface which can contain a matrix covered with aliphatic chains. This hydrophobic matrix can easily be covered with a lipidic layer by spontaneous fusion of liposomes injected into its contact. Olfactory receptors inserted in the liposomes or vesicles can thus be integrated into the biosensors. The ligands are thus analysed with regard to one or several different olfactory receptors.

The above methods make it possible to determine whether a compound activates or inhibits the receptors. In this embodiment, it is advantageous to use a known ligand which allows measurement by competition.

The invention also relates to a compound as yet unknown constituting a ligand of an olfactory receptor, identified and selected by the above process.

The receptors of the invention find applications in very varied domains such as:

- the food processing industry, for detection of aromas, quality control, analysis of samples.
- perfumery, for the analysis or comparison of perfumes,
- the environment, for detecting toxic substances, such as gases or for trapping odours.

The sequence data from this invention have been deposited with the DDBJ/EMBL/GenBank Data Libraries under accession numbers AF022649, AF073959-073989, AF127814-127907, and AF179716-179846.

- Other advantages and characteristics of the invention will become apparent by reading the following examples concerning the identification and cloning of olfactory receptor genes and pseudogenes of mouse and primates, and which refer to the attached drawings in which:
 - Figure 1 represents a schematic phylogeny tree of the primate species used in the present study and adapted from (32).
 - Figure 2 represents a comparison of the deduced protein OR sequences obtained from the different

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primate species characterized in this study. The dendogram was established using the PileUp program from the GCG Package. Percent ASI was determined by pairwise sequence comparisons using the Gap program and is indicated along the abscissa of the tree. Sequences from the literature are indicated by an asterisk. Human OR sequences derived from the use of the OR3B/OR5B primers and representing the main OR families were selected from (3, 13). Dog (CfOLF1 and its human counterpart HsOLF1; CfOLF2) and chicken sequences were selected from (4) and (7) respectively. OR families (greater than 40% ASI) are indicated by open circles and subfamilies (greater than 60% ASI) by open squares. The main family was arbitrarily named family 1 and subdivided in 2 groups of subfamilies, 1-I and 1-II (ovals). Group 1-II comprises subfamilies A and B. Beside the sequence names, black dots indicate sequences derived from the use of the OR3B/OR5B consensus primers, black squares those derived from the OR3.1/7.1 consensus primers, black rectangles indicate potentially functional genes (uninterrupted ORFs). In the case of HSA 912-93 rectangle and double asterisk), this sequence contains only one non-sense point mutation in human, but is potentially coding in other primates (13). Human, HSA; chimpanzee, PTR; gorilla, GGO; orangutan, PPY; gibbon, HLA; macaque, MSY; baboon, PPA; marmoset, CJA; squirrel-monkey, SSC and SBO; lemur, EFU and ERU; zebrafish, DRE (see Table 1).

- Table 1 represents an estimation of the fraction of pseudogenes in the OR gene repertoire of primate species and mouse. OR sequences were established by sequencing PCR products generated using consensus OR primers OR3B/OR5B and OR3.1/OR7.1 on genomic DNA. Data for human are derived from Rouquier et al. (3) and this study. The 3 zebrafish sequences characterized in this work are indicated. The average pseudogene percentage for each branch was estimated by summing the percentage of each species divided by the number of species.

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I. Materials and Methods.

I.1. Cloning and analysis of OR-like sequences in primates and mouse.

The isolation of OR-related sequences has been described elsewhere (3, 13). Briefly, 100 ng of genomic DNA from each species was subjected to PCR using consensus OR (OR5B (TM2), OR5B-OR3B primers) T(G/A)TC-3'; PMY(F/L) FL(S/A/T/G/C)NLS; OR3B (TM7), AG(A/G)C(A/T)(A/G)TAIATGAAIGG(A/G)TTCAICAT-3'; M(L/F/V/I)NPF(I/M)Y(S/C)L) (14). A second pair of consensus (OR3.1 (TM3), OR3.1-OR7.1 GCIATGGCITA(C/T)GA(C/T)(A/C)GITA-3'; AMAYD(S/R)Y; OR7.1 5'-(TM7), A(A/G)I(G/C)(A/T)(A/G)TA(A/G/T)AT(A/G)AAIGG(A/G)TT-3'; NPFIY(S/R/T/C/W)(L/F)) (15, 16), was also used to amplify primate OR sequences. PCR products were subcloned in the TA vector (InVitrogen), and recombinant clones were identified by PCR. Sequencing of the OR sequences was performed and sequences were assembled and analyzed as detailed elsewhere The following species were studied: human (Homo (3). sapiens, HSA), chimpanzee (Pan troglodytes, PTR), gorilla (Gorilla gorilla, GGO), orangutan (Pongo pygmaeus, PPY), gibbon (Hylobates lar, HLA), macaque (Macaca sylvanus, MSY), baboon (Papio papio, PPA), marmoset (Callithrix jacchus, CJA), squirrel-monkey (Saimiri sciureus, SSC, and Saimiri boliviensis, SBO), lemur (Eulemur fulvus, EFU, and Eulemur rubriventer, ERU), and mouse (Mus musculus domesticus, MMU). In addition, a few zebrafish (Danio rerio, DRE) sequences

Pairwise sequence comparisons and multiple alignments were performed using Gap and PileUp from the GCG package (Wisconsin Package version 8).

were characterized using primers OR3.1-OR7.1.

I.2. <u>Construction and screening of an OR-specific mouse sublibrary</u>.

Mouse OR clones obtained by PCR as described above were gridded in 96-well microtiter dishes (1536 clones in 8 plates). For hybridization screening, the clones were

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robot-spotted in duplicate on high-density filters described elsewhere (17). Approximately 90% of the clones were identified as OR genes. This library was screened to clones hybridizing human OR pseudogene identify to sequences. Human plasmid DNA probes were radiolabeled to a specific activity of 10^8-10^9 cpm/ μ g by random hexamer $(-32_{\rm P}) - dCTP$ priming (18)using (Amersham). Filter hybridizations were carried out under standard hybridization conditions (19), and exposed to Kodak X-ray film at -80°C. Three human OR probes were used: OR1-72, OR912-47, OR15-71 (DDBJ/GenBank accession numbers U86218, U86230, U86296 respectively).

II. Results.

II.1. <u>Isolation and analysis of primate OR</u> sequences.

To sample the OR genes in primate species, OR anthropoids and prosimians were randomly sequenced (Fig. 1). OR genes were obtained by PCR on genomic DNA from the different species using consensus OR primer pairs OR5B-OR3B and OR3.1-OR7.1 chosen respectively in the transmembrane domains TM2 and TM7, and TM3 and TM7. Except human, eighteen to thirty-five individual OR clones were sequenced per taxon. A total of 221 OR sequences, representing 10 species, was analyzed. These sequences are different groups in whose percentage distributed nucleotide sequence identity (NSI) ranges from ~35 to >99% (not shown). The corresponding amino-acid sequences were compared to a variety of OR sequences from the public databases and previous studies (3). All sequences have the characteristic features of olfactory receptors, with a heptahelical structure and conserved motifs as previously defined (1, 3, 14). The use of two pairs of consensus primers made our sampling representative of the OR gene repertoire. Primate sequences are distributed in 7 families (sequences that share >40% amino-acid identity (ASI) define a family), and 56 subfamilies (ASI>60%), with group 1-II of family 1 representing the zone of overlap of sequences

derived from using the two primer pairs (Fig. 2). Non-human primate OR genes are represented in 6 families and about 45 subfamilies. Numerous sequences are grouped in family 1 comprising subfamily 1A, the largest subfamily (57/221, 26%). Subfamily 1B is almost devoid of coding human OR sequences (Fig. 2). Subfamily 1A contains only human pseudogenes originating from chromosomes 14 and 19 (not shown) whereas subfamily 1B contains human pseudogenes lying on various chromosomes (not shown) (3). As the Applicant found previously for human (3), the amino-acid sequences deduced from the non-human primate sequences revealed many 2 and Table 1). Table 1 pseudogenes (Fig. information about the evolution of the pseudogene fraction along with the evolution of primates. Hominoids present the highest fraction of pseudogenes (39 to >70%, average ~50%). (macaque and baboon) have a lower Old world monkeys pseudogene fraction (20 to 35%, average 27%), while even fewer pseudogenes were found among the sequences derived from new world monkeys. Only one pseudogene (SBO64) was identified among the 49 sequences obtained from marmoset and two species of squirrel-monkey. In contrast, 37% of the prosimian lemur OR sequences were pseudogenes.

II.2. Sequence analysis of mouse OR sequences.

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To test whether mammals thought to be microsmatic or macrosmatic differ in the fraction of pseudogenes in their OR repertoire, OR sequences in the mouse genome were surveyed. A mouse sublibrary enriched for OR-related sequences amplified by PCR from the mouse genome was constructed (see materials and methods).

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Nineteen randomly selected mouse OR clones were sequenced. All 19 have an uninterrupted open-reading frame (ORF) and are potentially functional. These sequences group primarily in family 1 (not shown) and vary from ~52 to >99% NSI (not shown). In addition, in an attempt to bias in favor of selecting mouse OR pseudogenes, the Applicant searched for mouse OR sequences homologous to human pseudogenes. One member was chosen from three different OR pseudogene families: clones 1-72, 15-71 and 912-47 from chromosomes 1,

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15 and 11, respectively (3). Each of these genes belongs to one of the 3 main groups of human OR sequences and has accumulated a number of mutations such as stop codons and indel frameshifts (3). The amino-acid sequence identity between these three ranges from 31% to 41%.

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High density filters from the mouse OR sublibrary were then hybridized separately with the three human pseudogene probes at a high stringency. Fourteen clones were sequenced on both strands. These sequences showed 38% to 53% ASI to the human sequences used to select them, indicating that they are not the orthologs of the human pseudogenes. All have an uninterrupted ORF from TM2 to TM7 (not shown). Together, 33 mouse OR sequences were sequenced, none of which containing characteristic features of pseudogenes.

III. Discussion.

the basis for the differences in What is olfactory ability observed among mammals? Diverse reasons suggested that could account for differences, i.e. the size of the anatomical structures devoted to olfaction (olfactory epithelium, olfactory bulb, of structures), orthe number cortical families/subfamilies, and the total number and diversity of expressed OR genes. The olfactory epithelial surface of macrosmatic animals such as dogs is larger than microsmatic humans ((4) and references therein). other hand, using unique dog sequence probes that represent specific OR subfamilies and which will not cross-hybridize with other subfamilies, comparative analyses have been performed by Southern blot analysis among a panel of mammals including dog and human. This study indicates that the number of OR sequences per subfamily is similar microsmatic and macrosmatic animals (4). Recently the Applicant demonstrated that a high fraction (>70%) of the human OR genes have been mutated during evolution into pseudogenes (3). The Applicant found that chromosomes 7, 16 or 17 contained a high fraction of potentially coding OR sequences, whereas other chromosomes such as chromosome 3

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(3, 20) or 11 (3) contained primarily pseudogenes. Other studies on chromosome 17 (14, 21), and on chromosome 11 (22) identified 75% of the OR sequences which pseudogenes, support these observations. These findings led us to hypothesize that the number of functional OR genes could be correlated to the olfactory capability of a given animal. In an attempt to test this hypothesis, the OR gene repertoire of the main primate species, thought to be microsmatic, and of mouse, thought to be macrosmatic were sampled. The Applicant's analysis clearly indicates that from new world monkeys (see Fig. 1 and Table 1) hominoids, there is an increase during evolution of the percentage of OR pseudogenes from ~0 to ~70%, with the highest pseudogene content observed in gorilla, chimpanzee and human. Supporting this observation, during the course of this work, Sharon and colleagues (23) published a study about the evolution in primates of the OR genes orthologous to the human OR gene cluster located on chromosome 17p13.3 (14, 21). The authors conclude to a rapid decline (~10 Mya, corresponding to the radiation of hominoids) functional OR repertoire in mammals. In addition, Applicant showed in a recent study that this pool pseudogenes is still growing in human, which will probably evolve towards a minimal set of functional OR genes (13). It is therefore likely that there is a selective advantage for new world monkeys to retain a high proportion of functional OR genes whereas this advantage appears to be reduced in old world monkeys. The prosimian branch represented by two lemur species does not follow this rule and has accumulated a high fraction of OR pseudogenes (Table 1). This particular taxon is localized in Madagascar and is composed of diurnal (as and nocturnal (as Eulemur rubriventer) Eulemur fulvus) animals, both of which are thought to have evolved from a common ancestral species. The two species showed no striking difference in the OR pseudogene fraction suggesting that loss of functional OR genes preceded their divergence. despite the number of OR families Nevertheless, subfamilies presented in this study (Fig. 2), the collection of sequences of the present work represents a subset of OR

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genes and it is still possible that the fraction of functional OR genes and OR pseudogenes could be reversed in other segments of the OR family in different species. However, although some studies indicate that mouse or dog display better olfactory performances than human (10, 24), accurate experiments to compare the olfactory ability between the different primates species remain to be conducted to support our hypothesis.

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All OR sequences the Applicant derived from mouse are potentially coding. No pseudogenes were detected either by sequencing randomly selected OR sequences or by deliberately screening with human OR pseudogene probes. This indicates that the OR pseudogene content is either zero or restricted to rare examples in mouse (25).

Taken together, this study led us to hypothesize that the reduction of the sense of smell could correlate with the fraction of functional OR genes in the genome. This observation would probably result from the relaxation of the selective pressure exerted on the different species, i.e. as soon as the function becomes non-essential for the survival . or the social behavior of a particular species, the genes responsible for that function tend to accumulate deleterious Actually, it is likely that the different mutations. hypotheses evoked to explain the loss of function would be not exclusive, but that a parallel might exist between the reduction of the anatomical structures devoted to olfaction, the decrease in the number of functional OR genes, and the reduction of the sense of smell. This hypothesis is strongly supported by the fact that aquatic mammals such as dolphin which has a reduced olfactory apparatus, have only OR pseudogenes (15). These animals live in water and do not need to smell volatile odorants. Therefore, a parallel degeneration of the olfactory organs and the OR gene repertoire has occured probably due to the relaxation of the selective constraints. This sort of observation has also been made in the blind marsupial mole, in which degeneration accompanied by mutation is eyes interphotoreceptor retinoid binding protein gene, which is

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involved in the regeneration of rhodopsin in the visual cycle (26).

However, it is difficult to measure and compare the olfactory efficiency of different animal species. Various parameters such as the threshold of detection of odorants (sensitivity), the range of odors detectable and the discriminatory power (acuity) are key parts of the is uncertain to determine it olfactory ability. Thus precisely which of these parameters are taken in account when comparing two species, and therefore the origin of the olfactory deficiency of primates remains a controversial and difficult point to address. Furthermore, there is no data available in the literature comparing the olfactory ability between the different primate species studied in this work, and most of the few studies conducted to compare the performances of mouse or dog versus human concern either the threshold of detection of very few odorants (for example the n-amyl acetate (27)) or the observation that trained dogs are far better than human to detect hidden objects such as mines, drugs, or scavenged people after natural disasters (28, 29). None the less, if the fraction of OR pseudogenes has been estimated in mouse, it remains to be determined in dog.

The chromosomal distribution of the OR gene repertoire arose through multiple duplication rounds (3, 5, 20, 30, 31) giving rise to paralogous regions. Even though the number of duplication events may be different among the mammals, overall it appears that the number of OR genes was established before the divergence of mammals (4). This explains why by Southern analysis there is no striking difference in the number of OR genes of four different the sea lion, which has subfamilies between underdeveloped olfactory apparatus, and other mammals (4). On the other hand, the Southern blot approach does not reveal the functionality of the OR sequences, Applicant predicts that a large fraction of the sea lion OR genes could be pseudogenes as has been described for the dolphin (23). Similarly striking differences have been observed in the olfactory ability of different breeds of

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dogs (12). Despite the variations in the size of the olfactory epithelium of the differents breeds ((12) and references therein), it would be interesting to know what the biological basis is for the differences in performances observed between sight and scent hounds. One obvious possibility is loss of functional OR genes, but, given the recent origin of all modern dogs this explanation seems unlikely. Other explanations could be changes in behavior, or in expression brought about by the modification of a key master transcription factor or in the unusual mechanism that allows only one OR gene allele or the other to be expressed exclusively in any one epithelium cell.

Finally, the Applicant hypothesizes that the study of the evolution of the olfactory receptor gene repertoire through the determination of the pseudogene fraction, could mirror the evolution of the olfactory sensory function in micro- and macrosmatic mammals.

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	Species					
		•	Number of	300 %	0/ mandadana	Average %
,	Соштоп пате		sequences analyzed	% ORF	vo pseudogenes	pseudogenes
	Human	Homo sapiens (HSA)	66	30	70	٠
	Chimpanzee	Pan troglodytes (PTR)	21	52	. 48	
Hominoids	Gorilla	Gorilla gorilla (GGO)	18	20	50	% 0 <i>S</i>
	Orangutan	Pongo pygmaeus (PPY)	23	61	39	
	Gibbon	Hylobates lar (HLA)	22	59	41	
Old world monkeys	Macaque	Macaca sylvanus (MSY)	20	99	35	
	Baboon	Papio papio (PPA)	21	81	19	27 %
	٠					
	Marmoset	Callithrix jacchus (CJA)	.19	100	0	
New world monkeys	Squirrel-monkey	Saimiri scireus (SSC)	15	100	. 0	2 %
		Saimiri bolivensis (SBO)	15	93	7	
Prosimians	Lemur	Eulemur fulvus (EFU)	19	28	42	
	,	Eulemur rubriventer (ERU)	16	69	31	37 %
Rodents	Mouse	Mus musculus (MMU)	. 33	100	0	%0
			•	_		
Fish	Zebrafish	Danio rerio (DRE)	3	100	0	% 0

Toble 1

CLAIMS

1. Molecule of nucleic acid constituted by or comprising a sequence chosen among those represented in the list of sequences in the appendix under the numbers SEQ ID No. 3, SEQ ID No. 12, SEQ ID No. 21, SEQ ID No. 22, SEQ ID 5 No. 23, SEQ ID No. 24, SEQ ID No. 25, SEQ ID No. 26, SEQ ID No. 27, SEQ ID No. 28, SEQ ID No. 29, SEQ ID No. 30, SEQ ID No. 31, SEQ ID No. 36, SEQ ID No. 37, SEQ ID No. 40, SEQ ID No. 41, SEQ ID No. 42, SEQ ID No. 43, SEQ ID No. 52, SEQ ID No. 53, SEQ ID No. 58, SEQ ID No. 59, SEQ ID No. 60, SEQ ID 10 No. 61, SEQ ID No. 64, SEQ ID No. 67, SEQ ID No. 72, SEQ ID No. 73, SEQ ID No. 76, SEQ ID No. 81, SEQ ID No. 88, SEQ ID No. 111, SEQ ID No. 114, SEQ ID No. 117, SEQ ID No. 118, SEQ ID No. 119, SEQ ID No. 120, SEQ ID No. 121, SEQ ID No. 122, SEQ ID No. 123, SEQ ID No. 142, SEQ ID No. 151, SEQ ID No. 15 152, SEQ ID No. 171, SEQ ID No. 188, SEQ ID No. 205, SEQ ID No. 212, SEO ID No. 215, SEQ ID No. 216, SEQ ID No. 221, SEQ ID No. 230, SEQ ID No. 231, SEQ ID No. 232, SEQ ID No. 233, SEQ ID No. 238, SEQ ID No. 239, SEQ ID No. 244, SEQ ID No. 251, SEQ ID No. 258, SEQ ID No. 259, SEQ ID No. 260, SEQ ID 20 No. 261, SEQ ID No. 272, SEQ ID No. 279, SEQ ID No. 282, SEQ ID No. 291, SEQ ID No. 292, SEQ ID No. 313, SEQ ID No. 314, SEO ID No. 317, SEQ ID No. 324, SEQ ID No. 327, SEQ ID No. 350, SEQ ID No. 363, SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEO ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 25 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEO ID No. 50, SEQ ID No. 54, SEQ ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 30 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, SEQ ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, 35 SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 155, SEQ ID No. 157, SEQ

ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEQ ID No. 180, SEQ ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 193, SEQ ID No. 195, SEQ ID No. 197, 5 SEQ ID No. 199, SEQ ID No. 201, SEQ ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEO ID No. 240, SEQ ID No. 242, SEQ ID No. 245, SEQ ID No. 10 247, SEQ ID No. 249, SEQ ID No. 252, SEQ ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266, SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ ID No. 289, SEQ ID No. 293, SEQ ID 15 No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEQ ID No. 325, SEQ ID No. 328, SEQ ID No. 330, SEQ ID No. 332, SEQ ID No. 334, SEQ 20 ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ ID No. 355, SEQ ID No. 357, SEQ ID No. 359, SEQ ID No. 361, SEQ ID No. 364, SEQ ID No. 366, SEQ ID No. 368, SEQ ID No. 370, SEQ ID No. 372, SEQ ID No. 374, 25 SEQ ID No. 376, SEQ ID No. 378, SEQ ID No. 380, SEQ ID No. 382, SEQ ID No. 384, SEQ ID No. 386, SEQ ID No. 388, SEQ ID No. 390, SEQ ID No. 392, SEQ ID No. 394, SEQ ID No. 396, SEQ ID No. 398, SEQ ID No. 400, SEQ ID No. 402, SEQ ID No. 404, SEQ ID No. 406, SEQ ID No. 408, SEQ ID No. 410, SEQ ID No. 30 412, SEQ ID No. 414, SEQ ID No. 416, SEQ ID No. 418, SEQ ID No. 420, SEQ ID No. 422, SEQ ID No. 424, SEQ ID No. 426, SEQ ID No. 428 and SEQ ID No. 430.

2. Molecule of nucleic acid according to claim
1, wherein said sequence is an encoding nucleic sequence for
an olfactory receptor or for a fragment of an olfactory
receptor and is chosen among those represented in the list

of sequences in the appendix under the numbers SEQ ID No. 1, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17, SEQ ID No. 19, SEQ ID No. 32, SEQ ID No. 34, SEQ ID No. 38, SEQ ID No. 44, SEQ ID No. 46, SEQ ID No. 48, SEQ ID No. 50, SEQ ID No. 54, SEQ 5 ID No. 56, SEQ ID No. 62, SEQ ID No. 65, SEQ ID No. 68, SEQ ID No. 70, SEQ ID No. 74, SEQ ID No. 77, SEQ ID No. 79, SEQ ID No. 82, SEQ ID No. 84, SEQ ID No. 86, SEQ ID No. 89, SEQ ID No. 91, SEQ ID No. 93, SEQ ID No. 95, SEQ ID No. 97, SEQ ID No. 99, SEQ ID No. 101, SEQ ID No. 103, SEQ ID No. 105, 10 SEO ID No. 107, SEQ ID No. 109, SEQ ID No. 112, SEQ ID No. 115, SEQ ID No. 124, SEQ ID No. 126, SEQ ID No. 128, SEQ ID No. 130, SEQ ID No. 132, SEQ ID No. 134, SEQ ID No. 136, SEQ ID No. 138, SEQ ID No. 140, SEQ ID No. 143, SEQ ID No. 145, SEQ ID No. 147, SEQ ID No. 149, SEQ ID No. 153, SEQ ID No. 15 155, SEQ ID No. 157, SEQ ID No. 159, SEQ ID No. 161, SEQ ID No. 163, SEQ ID No. 165, SEQ ID No. 167, SEQ ID No. 169, SEQ ID No. 172, SEQ ID No. 174, SEQ ID No. 176, SEQ ID No. 178, SEO ID No. 180, SEQ ID No. 182, SEQ ID No. 184, SEQ ID No. 186, SEQ ID No. 189, SEQ ID No. 191, SEQ ID No. 193, SEQ ID 20 No. 195, SEQ ID No. 197, SEQ ID No. 199, SEQ ID No. 201, SEQ: ID No. 203, SEQ ID No. 206, SEQ ID No. 208, SEQ ID No. 210, SEQ ID No. 213, SEQ ID No. 217, SEQ ID No. 219, SEQ ID No. 222, SEQ ID No. 224, SEQ ID No. 226, SEQ ID No. 228, SEQ ID No. 234, SEQ ID No. 236, SEQ ID No. 240, SEQ ID No. 242, SEQ 25 ID No. 245, SEQ ID No. 247, SEQ ID No. 249, SEQ ID No. 252, SEO ID No. 254, SEQ ID No. 256, SEQ ID No. 262, SEQ ID No. 264, SEQ ID No. 266, SEQ ID No. 268, SEQ ID No. 270, SEQ ID No. 273, SEQ ID No. 275, SEQ ID No. 277, SEQ ID No. 280, SEQ ID No. 283, SEQ ID No. 285, SEQ ID No. 287, SEQ ID No. 289, 30 SEQ ID No. 293, SEQ ID No. 293, SEQ ID No. 295, SEQ ID No. 297, SEQ ID No. 299, SEQ ID No. 301, SEQ ID No. 303, SEQ ID No. 305, SEQ ID No. 307, SEQ ID No. 309, SEQ ID No. 311, SEQ ID No. 315, SEQ ID No. 318, SEQ ID No. 320, SEQ ID No. 322, SEO ID No. 325, SEQ ID No. 328, SEQ ID No. 330, SEQ ID No. 35 332, SEQ ID No. 334, SEQ ID No. 336, SEQ ID No. 338, SEQ ID No. 340, SEQ ID No. 342, SEQ ID No. 344, SEQ ID No. 346, SEQ ID No. 348, SEQ ID No. 351, SEQ ID No. 353, SEQ ID No. 355,

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3. Molecule of encoding nucleic sequence for the olfactory receptors or for fragments of olfactory receptors whose amino acid sequences are represented in the list of sequences in the appendix under the numbers SEQ ID No. 2, 15 SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 18, SEQ ID No. 20, SEQ ID No. 33, SEO ID No. 39, SEQ ID No. 45, SEQ ID No. 47, SEQ ID No. 49, SEQ ID No. 51, SEQ ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ 20 ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, 25 SEO ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135, SEQ ID No. 137, SEQ ID No. 139, SEQ ID No. 141, SEQ ID No. 144, SEQ ID No. 146, SEQ ID No. 148, SEQ ID No. 150, SEQ ID No. 154, SEQ ID No. 156, SEQ ID No. 158, SEQ ID No. 160, SEQ ID No. 162, SEQ ID No. 164, SEQ ID No. 166, SEQ ID No. 168, SEQ ID No. 170, SEQ ID 30 No. 173, SEQ ID No. 175, SEQ ID No. 177, SEQ ID No. 179, SEQ ID No. 181, SEQ ID No. 183, SEQ ID No. 185, SEQ ID No. 187, SEQ ID No. 190, SEQ ID No. 192, SEQ ID No. 194, SEQ ID No. 196, SEQ ID No. 200, SEQ ID No. 202, SEQ ID No. 204, SEQ ID No. 209, SEQ ID No. 211, SEQ ID No. 214, SEQ ID No. 218, SEQ 35 ID No. 220, SEQ ID No. 223, SEQ ID No. 225, SEQ ID No. 227, SEQ ID No. 229, SEQ ID No. 235, SEQ ID No. 237, SEQ ID No. 241, SEQ ID No. 243, SEQ ID No. 246, SEQ ID No. 248, SEQ ID

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No. 250, SEO ID No. 253, SEQ ID No. 255, SEQ ID No. 257, SEQ ID No. 263, SEQ ID No. 265, SEQ ID No. 267, SEQ ID No. 269, SEQ ID No. 271, SEQ ID No. 274, SEQ ID No. 276, SEQ ID No. SEQ ID No. 278, SEQ ID No. 281, SEQ ID No. 284, SEQ ID No. 286, SEQ ID No. 288, SEQ ID No. 290, SEQ ID No. 294, 296, SEQ ID No. 298, SEQ ID No. 300, SEQ ID No. 302, SEQ ID No. 304, SEQ ID No. 306, SEQ ID No. 308, SEQ ID No. 310, SEQ ID No. 312, SEQ ID No. 316, SEQ ID No. 319, SEQ ID No. 321, SEQ ID No. 323, SEQ ID No. 326, SEQ ID No. 329, SEQ ID No. 331, SEQ ID No. 333, SEQ ID No. 335, SEQ ID No. 337, SEQ ID No. 339, SEQ ID No. 341, SEQ ID No. 343, SEQ ID No. 345, SEQ ID No. 347, SEQ ID No. 349, SEQ ID No. 352, SEQ ID No. 354, SEQ ID No. 356, SEQ ID No. 358, SEQ ID No. 360, SEQ ID No. 362, SEO ID No. 365, SEO ID No. 367, SEQ ID No. 369, SEQ ID No. 371, SEQ ID No. 373, SEQ ID No. 375, SEQ ID No. 377, SEQ ID No. 379, SEQ ID No. 381, SEQ ID No. 383, SEQ ID No. 385, SEQ ID No. 387, SEQ ID No. 389, SEQ ID No. 391, SEQ ID No. 393, SEQ ID No. 395, SEQ ID No. 397, SEQ ID No. 399, SEQ ID No. 401, SEQ ID No. 403, SEQ ID No. 405, SEQ ID No. 407, SEQ ID No. 409, SEQ ID No. 411, SEQ ID No. 413, SEQ ID No. 415, SEQ ID No. 417, SEQ ID No. 419, SEQ ID No. 421, SEQ ID No. 423, SEQ ID No. 425, SEQ ID No. 427, SEQ ID No. 429 and SEQ ID No. 431.

4. A purified olfactory receptor constituted by 25 or comprising the sequence of amino acids chosen among those represented in the list of amino acid sequences under the numbers SEQ ID No. 2, SEQ ID No. 5, SEQ ID No. 7, SEQ ID No. 9, SEQ ID No. 11, SEQ ID No. 14, SEQ ID No. 16, SEQ ID No. 30 18, SEQ ID No. 20, SEQ ID No. 33, SEQ ID No. 39, SEQ ID No. 45, SEO ID No. 47, SEO ID No. 49, SEO ID No. 51, SEO ID No. 55, SEQ ID No. 57, SEQ ID No. 63, SEQ ID No. 66, SEQ ID No. 69, SEQ ID No. 71, SEQ ID No. 75, SEQ ID No. 78, SEQ ID No. 80, SEQ ID No. 83, SEQ ID No. 85, SEQ ID No. 87, SEQ ID No. 90, SEQ ID No. 92, SEQ ID No. 94, SEQ ID No. 96, SEQ ID No. 35 98, SEQ ID No. 100, SEQ ID No. 102, SEQ ID No. 104, SEQ ID No. 106, SEQ ID No. 108, SEQ ID No. 110, SEQ ID No. 113, SEQ ID No. 116, SEQ ID No. 127, SEQ ID No. 131, SEQ ID No. 135,

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- 5. A polyclonal or monoclonal antibody directed against at least one receptor according to claim 4 or a derivative or a fragment thereof.
- 5 6. A vector comprising at least one molecule of nucleic acid according to one or the other of Claims 1 or 3, advantageously associated with control sequences.
- 7. Production process of a receptor according to claim 4, comprising the following steps:
 - transferring a molecule of nucleic acid according to one or the other of claims 2 or 3 or a vector according to Claim 6 into a host,
 - cultivating said cellular host in conditions allowing production of the protein constituting the receptor,
 - isolating said proteins, by all appropriate means.
 - 8. Expression process of a receptor according to claim 4 in a host, comprising the following steps:
 - transferring a molecule of nucleic acid according to one or the other of claims 2 or 3 or a vector according to Claim 6 into a host,
 - cultivating said host in conditions allowing expression of said receptors at the surface of the host.
 - 9. A host transformed by a molecule of nucleic acid according to one or other of claims 2 or 3 or by a vector according to Claim 6.
 - 10. Screening procedure of compounds capable of constituting ligands of a receptor according to claim 4, wherein the said compounds are put into contact one or several of said receptors then the affinity between said compound and said receptor is measured by all appropriate means.

- 11. A membrane on which one or several receptors are fixed according to claim 4 useful for applying a process according to claim 10.
- 5 12. A compound constituting a ligand of an olfactory receptor, identified and selected by the process according to claim 10.
- 13. Utilisation of a receptor according to claim 4, of a host according to claim 9 or of a membrane according to claim 11, for the detection of aromas, quality control, sample analysis, analysis or comparison of perfumes, detection of toxic substances, or the trapping

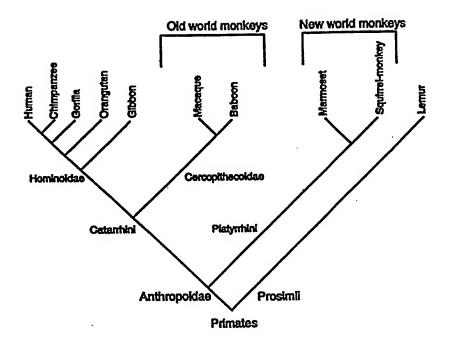


Figure 1

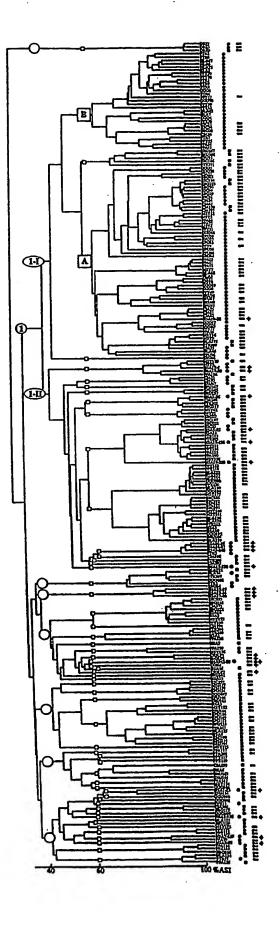


FIGURE 1

SEQUENCE LISTING

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<213>	Papio har	nadryas											·
<220>													
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<222>	(1)(649))										•	
<223>	Taxon. = 5	9557; ger	ne = PPA	13; P	Acces	sion	DDE	J/EM	iBL/C	enBa	ınk =	AF12	27814
<220>	•		•							•	•		
<221>											1		
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<223>	Product :	= olfacto	ory rece	ptor									
<400>	1												
c tgg	gtt gac a	tc tgt ti	cc agc a	.cc to	gc at	c gt	c cc	c aa	ig at	g ct	g gt	J .	49
Trp	Val Asp I	le Cys Pl	ne Ser I	hr Cy			al Pr	o Ly	s Me			L '	
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	•												0.5
	c cag acc												97
Asn Il	e Gln Thr	Lys Asn	Lys Thr		Ser	Tyr	Met	Asp		Leu	Thr		
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		•				_							4.45
cag gt	c tat ttc	tcc atg	ttt ttt	cct	att	ctg	ggc	aca	cta	CTC	ctg		145
Gln Va	l Tyr Phe	Ser Met		Pro	тте	Leu	GIĀ		ьеп	ьеп	ren		•
	35		40					45					
	.	.									a n a		193
	g atg gcc												133
	l Met Ala	TYI ASD	55	vai	ALA	val	60	птэ	FIU.	пеп	mis	•	
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***	a acc atc	2ta 22a	CCC CC	, ata	tat	aac	ctc	cta	att	+++	atc		241
	e Thr Ile												241
65	e ini ite	70	TTO AL	, Deu	. Cys	75	Deu	Dea	VUL	1110	80	•	
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aca to	g ctc att	ant atc	ato aco	ı taa	ctc	ctc	cat.	att	tet	cta	ato		289
	p Leu Ile											٠.	
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		0.5											
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	s Leu Thr											٠.	
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gaa ct	g aca cat	atc ctc	cag ct	a acc	tac	tct	gat	acc	ttc	cta	aac		385
_	ou Thr His												
	115		12		-		- 2	125					
age ag	g ttg ata	tat gtt	atg ac	g ggt	gta	cta	ggc	gtt	ttt	ccc	ctc		433
-50 41		•				- 3	20-						

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Ser	Thr 130	Leu	Ile	Tyr	Val	Met 135	Thr	Gly	Val	Leu	Gly 140	Val	Phe	Pro	Leu		
ctt Leu 145	Gly ggg	atc Ile	att Ile	ttc Phe	tct Ser 150	tat Tyr	tca Ser	cga Arg	atc Ile	gct Ala 155	tca Ser	tcc Ser	ata Ile	agg Arg	aag Lys 160		481
atg Met	tcc Ser	tca Ser	tct Ser	ggg Gly 165	gga Gly	aaa Lys	gag Glu	aaa Lys	gca Ala 170	ctt Leu	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser	•	529
												att Ile					577
ttc Phe	act Thr	tct Ser 195	gcg Ala	gtg Val	act Thr	cat His	tct Ser 200	tcc Ser	cag Gln	aac Asn	atc Ile	tcc Ser 205	gtg Val	gcc Ala	tcg Ser		625
	atg Met 210																649
	1> : 2> : 3> : 0> : 1> : 2> : 3> :	Papio misc (1).	_fea .(64	ture 9)		ne =	PPA	13;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF1	27814
Trp	Val	Asp	Ile	Cys 5	Phe	Ser	Thr	Cys	11e 10	Val	Pro	Lys	Met	Leu 15	Val		
Asn	Ile	Gln	Thr 20	Lys	Asn	Lys	Thr	Ile 25	Ser	Tyr	Met	Asp	Cys 30	Leu	Thr		
Glr	Val	Tyr 35	Phe	Ser	Met	Phe	Phe 40	Pro	Ile	Leu	Gly	Thr 45	Leu	Leu	Leu		
Thr	Val	Met	Ala	Тут	· Asp	Arg 55	Phe	val	. Ala	Val	Суs 60	His	Pro	Leu	His		
Туз 65	: Ile	. Thr	Ile	Met	70	Pro	Arg	, Leu	ı Cys	6 Gly 75	Leu	ı Lev	Val	Phe	Val 80		

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met

85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 3

<211> 642

<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

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AF127815

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cgcatgtatg gaaagtctgc tectggctgt gatggcctat gaccggtttg tggccatctg 180

tcacccccta cactgcccag tcatcatgaa cccacgcctt tgtggctttt tagttttggt 240

gtottttott ottagootgt tggattocca gotacacaat ttgattgtgt tacaacttac 300

ctgcttcaat ga	atgtggaaa tct	ctaaatt ttt	ctgtgac ccttct	caac ttctcaatcc	360
tagectgete to	gacacataa cat	agtcgta tat	tttattg gtacca	atatt tggttttctt	420
cctctctcag gg	gatcctttt ctt	ttactat aaa	attgttt cctcca	attcc gagagttcgc	480
tetteaggta g	gaagtataa ago	cttctcc acc	tgcagct ctcaco	ettte agttgtttge	540
ttattttatg ga	aacagccct tgg	gagggtac ctc	agttcag ctgtc	ctct ccccccagg	600
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Asn Ile Gln	acc aag aac a Thr Lys Asn I 20	aaa acg att Lys Thr Ile 25	tct tac atg g Ser Tyr Met A	ac tgc ctc acc sp Cys Leu Thr 30	97
				ca cta ctc ctg hr Leu Leu Leu 5	·145
	Ala Tyr Asp			ac ccc ctg cac is Pro Leu His	193
				tg gtt ttt gtc eu Val Phe Val 80	241
				tt tct ctg atg le Ser Leu Met 95	289
aca cat cta Thr His Leu			gaa att gga g		337

gaa ctg Glu Leu															385
agc acg Ser Thr	Leu			Val											433
ctt ggg Leu Gly 145															481
atg tco Met Ser	tca Ser	tct Ser	ggg Gly 165	gga Gly	aaa Lys	gag Glu	aaa Lys	gca Ala 170	ctt Leu	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser	529
cac cto															577
ttc act															625
gtg ato Val Met 210	Tyr				_										649
<210> <211> <212> <213>	216 PRT	o ha	madr	yas											
<220> <221> <222> <223>	(1).	. (64	9)		ne =	PPA	15;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF127816
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Asn Il	e Glr	Thr 20	Lys	Asn	Lys	Thr	Ile 25	Ser	Тух	Met	Asp	Cys 30	Leu	Thr	
Gln Va	1 Tyr 35	: Phe	Ser	Met	. Phe	Phe 40	Pro	Ile	. Lev	Asp	Thr 45	Leu	. Leu	Leu	

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50 55 60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 6

<211> 649

<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA; Accession DDBJ/EMBL/GenBank = AF27817

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<222> (2)..(649)

<223> Product = olfactory receptor

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aac ato Asn Ile															97
cag gto Gln Val															145
acc gtg Thr Val															193
tac acc Tyr Th:															241
tcc tgg Ser Tr															289
ttg agg	J Leu	Ser 100	Phe	Cys	Ile	Lys	Met 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys	337
gat ct Asp Le	1 Pro 115	Glu	Val	Leu	Lys	Leu 120	Ala	Cys	Ser	Asp	Thr 125	Phe	Ile	Asn	385
aat gt Asn Va 13	l Val	Ile	Tyr	Phe	Ala 135	Thr	Gly	Ile	Leu	Ala 140	Val	Ile	Pro	Phe	433
act gg Thr Gl 145	y Ile	Leu	Phe	Ser 150	Tyr	Tyr	ГЛЗ	Ile	Val 155	Phe	Ser	Val	Leu	Arg 160	481
att tc Ile Se	r Ser	Ala	Gly 165	Gly	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser	529
cac ct His Le	u Ser	Met 180	Val	Ser	Leu	Phe	Tyr 185	Gly	Thr	Gly	Leu	Gly 190	Val	Tyr	577
ctc ag Leu Se	r Ser 195	Ala	Ala	Ile	Pro	Ser 200	Ser								625
gtg at Val Me															649

210 215

<210> 7

<211> 216

<212> PRT

<213> Papio hamadryas

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<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9557; gene = PPA; Accession DDBJ/EMBL/GenBank = AF27817

<400> 7

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Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His 50 55 60

Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val 85 90 95

Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys 100 105 110

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn 115 120 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe 130 135 140

Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg 145 150 155 160

Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175 His Leu Ser Met Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Ile Pro Ser Ser Arg Thr Ser Leu Val Ala Ser 195 200 205

Val Met Tyr Thr Met Val Thr Pro 210 215

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<222	> (2)	(649)												
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c ta	a at	t ga	c at	c tg	t tt	c ag	c ac	c tg	c at	c gt	c cc	c aa	g at	g ct	g gtg	49
Tr	υ Va	ıl As	r II	e Cy	s Ph	e Se	r Th	r Cy	s Il	e Va	1 Pr	о Ьу	s Me	t Le	u Val	
1			•	5					10					15		
_																
aac	atc	caq	acc	aag	aac	aaa	acg	att	tct	tac	atg	gac	tgc	ctc	acc	97
Asn	Ile	Gln	Thr	Lvs	Asn	Lys	Thr	Ile	Ser	Tyr	Met	Asp	Cys	Leu	Thr	
			20	-		_		25					30			
			_													
car	atc	tat	ttc	tcc	atg	ttt	ttt	cct	att	ctg	gac	aca	cta	ctc	ctg	145
Gln	Val	Tvr	Phe	Ser	Met	Phe	Phe	Pro	Ile	Leu	Asp	Thr	Leu	Leu	Leu	
0111	V (4.2.	35					40				-	45				
		J J														
200	ata	ata	מככ	tat	gac	caa	ttt	ata	αcc	atc	tac	cac	ccc	ctg	cac	193
mh~	yry val	Mot	λla	Tarr	Asp	Δra	Phe	Val	Ala	Val	Cvs	His	Pro	Leu	His	
1111	50	Hec	ALG	131	тор	55					60			-		
	50					55					••					
				2+4	aac		cac	ctc	tat	ממכ	ctc	cta	att	ttt	atc	241
tat	ata	mb	TIO	Mot	Asn	Dro	724	Lou	Cyc	Clv	Leu	Tien	Val	Phe	Val	
	тте	THE	TTE	met	70	PIO	ALG	Dea	Cys	75	DCu.		· · · ·		80	
65					70					, ,						
						- 4				ata	 +	-++	tat	a+a	ata	289
acg	tgg	ctc	att	ggt	gtc	atg	aca	Coc	Ton	Tou	uic	TIO	Cor	Lou	Mot	200
Thr	Trp	Leu	TTE		Val	met	Thr	Ser		Leu	urs	116	Ser	95	Mec	
				85					90					90		
										- 4-2						337
aca	cat	cta	acc	ttc	tgt	aaa	gat	ttt	gaa	att	cca	cat	כככ	כנכ	Lgc	331
Thr	His	Leu		Phe	Cys	Lys	qaA		Glu	TTE	Pro	Hls		rne	cys	
			100					105					110			

					ctc Leu											385
					gtt Val											433
					tct Ser 150											481
					gga Gly											529
					tct Ser											577
					act Thr											625
	_		_		gtt Val										,	649
<21: <21: <21: <21: <22:	1> : 2> : 3> :	9 216 PRT Papi	o ha	madr	yas		,									
	1> 1 2> 3> '	(1).	_fea .(64: n =	9)		ne =	PPA	41;	Acce	ssio:	n DD	BJ/E	MBL/	GenB	ank =	AF127818
Trp			Ile	Cys 5	Phe	Ser	Thr	Cys	Ile 10	Val	Pro	Lys	Met	Leu 15	Val	
Asn	Ile	Gln	Thr 20	Lys	Asn	Lys	Thr	Ile 25	Ser	Tyr	Met	Asp	Суs 30	Leu	Thr	
Gln	Val	Tyr 35	Phe	Ser	Met	Phe	Phe 40	Pro	Ile	Leu	Asp	Thr 45	Leu	Leu	Leu	

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 10

<211> 649

<212> DNA

<213> Papio hamadryas

<220>

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<222> (1)..(649)

<223> Taxon = 9557; gene = PPA42; Accession DDBJ/EMBL/GenBank = AF127819

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<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 10

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_	_	_	_		_						tgc Cys 60					193
Tyr 65	Ala	Thr	Ile	Met	Ser 70	Pro	Arg	Leu	Cys	Gly 75	ctg Leu	Leu	Val	Gly	Val 80	241
					_						cac His					289
Ala	Arg	Leu	Val 100	Phe	Cys	Gly	Ser	His 105	Glu	Val	cct Pro	His	Tyr 110	Phe	Cys	337
Asp	Leu	Thr 115	Pro	Ile	Leu	Arg	Leu 120	Ser	Cys	Thr	gac Asp	Thr 125	Ser	Val	Asn	3,85
Arg	Ile 130	Phe	Ile	Leu	Ile	Val 135	Ala	Gly	Met	Val	ata Ile 140	Ala	Thr	Pro	Phe	433
Ile 145	Cys	Ile	Leu	Ala	Ser 150	Tyr	Ala	Arg	Ile	Leu 155	gcg	Ala	Ile	Met	Lys 160	481
Val	Pro	Ser	Ala	Gly 165	Gly	Arg	Lys	Lys	Ala 170	Phe	tcc Ser	Thr	Cys	Ser 175	Ser	529
His	Leu	Ser	Val 180	Val	Ala	Leu	Phe	Туг 185	Gly	Thr	acc	Ile	Gly 190	Val	Tyr	577
Leu	Cys	Pro 195	Ser	Ser	Val	Arg	Thr 200	Ala		_	gag Glu		-		_	625
			aca Thr													649

215 210

<210> 11

<211> 216

<212> PRT

<213> Papio hamadryas

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<221> misc_feature

<222> (1)..(649)
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<400> 11

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Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr 30 25

Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile 35 40

Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val 65 70 75

Pro Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met 90

Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys 105

Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn 115 120

Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe 135 130

Ile Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Ala Ala Ile Met Lys 155 150

Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser 170

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180 185 190

Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala 195 200 205

Val Met Tyr Thr Ala Val Thr Pro 210 215

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<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

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<221 <222		DS (2)	(649))												
			ict =		acto	ry r	ecer	ptor								
<400		.3 :=		c to	++ ++	t at	a ta	יר פי	יר פנ	יד מו	٠, ٥,	ro aa	no at	a ci	g gtg	49
		_	_	_		_	_					-			eu Val	
1				5					10)				1!	5	
aac	atc	cag	aca	cag	agc	aga	gtc	atc	acc	tat	gca	ggc	tgc	atc	acc	97
Asn	Ile	Gln	Thr	·Gln	Ser	Arg	Val		Thr	Tyr	Ala	Gly		Ile	Thr	
		•	20					25					30			
_	_	-	ttt							_	_					145
Gln		Cys 35	Phe	Phe	Ile	Phe	Phe 40	Ala	Gly	Leu	Asp	Ile 45	Phe	Met	Leu	
		,,,					30									
		_	gcc Ala		_				_	_	_			_		193
THE	50	met	АТА	TYL	qsA	55	rne	vai	ALG		60	птэ	PIU	пец	urs	
											•					0.44
	-	-	acc Thr	-												241
65					70				•	75					80	
tee	taa	atc	atg	agt	acc	cta	aat	tct	t.ca	tta	caa	agc	tta	ato	gta	289
			Met	_							_				_	
				85					90					95		
ttg	cac	ctt	tcc	ttc	tgt	gca	gac	ttg	gaa	att	ccc	cac	ttt	ttc	tgt	337
Leu	His	Leu	Ser 100	Phe	Суѕ	Ala	Asp	Leu 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys	
			100					103					110			
-			cag Gln													385
GIU	rea	115	GIII	vai	vaı	urs	120	Ala	Cys	per	ASP	125	·	пеп	ASII	
							44						·			422
-	_		atg Met		_	_								-		433
	130			_		135					140					
tct	ggg	atc	ctt	tat	tct	tat	tct	aag	atc	gtt	tcc	tcc	ata	cgt	gga	481
	Gly	Ile	Leu	Tyr		Tyr	Ser	Lys	Ile		Ser	Ser	Ile	Arg	_	
145					150					155					160	
	_		gct	_		_			_				-	_		529
Thr	Ser	Ser	Ala	Gln 165	Gly	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Суѕ	Ala 175	Ser	
				200					-,0					J. 1 J		
			gtt Val										-			577
ura	nen	ser	180	A CT T	ne1	₽₽U	rne	185	⊕±Ã	TILL	neu	มสน	190	vaT	TÄT	

ttt agt tct gct gca acc cgt aac tca cac tca agt gct gca gcc tcg Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser 195 200 649 gtg atg tac act gtg gtt acc ccc Val Met Tyr Thr Val Val Thr Pro 210 <210> 14 <211> 216 <212> PRT <213> Papio hamadryas <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9557; gene = PPA68; Accession DDBJ/EMBL/GenBank = AF127821 <400> 14 Phe Ile Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 10 5 Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr 25 20 30 Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu 35 40 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 70 75 Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val 90 85 Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu 130 135 140

		17	1 € 1/1100/02017
Ser Gly Ile Leu 145	Tyr Ser Tyr 150	Ser Lys Ile Val Se 155	r Ser Ile Arg Gly 160
	Gln Gly Lys 165	Tyr Lys Ala Phe Se 170	r Thr Cys Ala Ser 175
His Leu Ser Val 180	Val Ser Leu	Phe Tyr Gly Thr Le 185	u Leu Gly Val Tyr 190
Phe Ser Ser Ala 195	Ala Thr Arg	Asn Ser His Ser Se 200	r Ala Ala Ala Ser 205
Val Met Tyr Thr 210	Val Val Thr 215	Pro	
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<pre><223> Taxon = 9 <220> <221> CDS <222> (2)(649 <223> Product = <400> 15 c ttc ata gac at Phe Ile Asp II 1 aac atc cag aca</pre>	e) 2557; gene = 2) colfactory : tc tgt ttt gi le Cys Phe Va 5 cag agc aga	receptor tg tcc acc act gtc al Ser Thr Thr Val	ccg aag atg ctg gtg 49 Pro Lys Met Leu Val 15
<pre><223> Taxon = 9 <220> <221> CDS <222> (2)(649 <223> Product = <400> 15 c ttc ata gac at Phe Ile Asp I 1 aac atc cag aca Asn Ile Gln Thr 20 cag atg tgc ttt</pre>	cag agc aga Gln Ser Arg	receptor tg tcc acc act gtc al Ser Thr Thr Val 10 gtc atc acc tat go Val Ile Thr Tyr Al	ccg aag atg ctg gtg 49 Pro Lys Met Leu Val 15 a ggc tgc atc acc 97 a Gly Cys Ile Thr 30
<pre><223> Taxon = 9 <220> <221> CDS <222> (2)(649 <223> Product = <400> 15 c ttc ata gac at Phe Ile Asp II aac atc cag aca Asn Ile Gln Thr</pre>	cag agc aga Gln Ser Arg ttc ata ttc Phe Ile Phe ttt gac cgg	receptor tg tcc acc act gtc al Ser Thr Thr Val 10 gtc atc acc tat gc Val Ile Thr Tyr Al 25 ttt gcg gga ctg ga Phe Ala Gly Leu As	ccg aag atg ctg gtg 49 Pro Lys Met Leu Val 15 a ggc tgc atc acc 97 a Gly Cys Ile Thr 30 at atc ttt atg ctg 145 ap Ile Phe Met Leu 45 gt cac ccc ctg cac 193 as His Pro Leu His
<pre><223> Taxon = 9 <220> <221> CDS <222> (2)(649 <223> Product = <400> 15 c ttc ata gac at Phe Ile Asp I aac atc cag aca Asn Ile Gln Thr</pre>	cag agc aga Gln Ser Arg ttc ata ttc Phe Ile Phe ttt gac cgg Phe Asp Arg 55 atg aac ccc	receptor tg tcc acc act gtc al Ser Thr Thr Val 10 gtc atc acc tat gc Val Ile Thr Tyr Al 25 ttt gcg gga ctg ga Phe Ala Gly Leu As 40 ttt gtg gcc atc tc Phe Val Ala Ile C	ccg aag atg ctg gtg 49 Pro Lys Met Leu Val 15 a ggc tgc atc acc 97 a Gly Cys Ile Thr 30 at atc ttt atg ctg 145 pp Ile Phe Met Leu 45 gt cac ccc ctg cac 193 rs His Pro Leu His cg ctg gtt ctg gcg 241

WO 01/46262		18	PCT/IB00/02017
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Tyr Thr Val Thr Met Asn Pro Lys Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

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Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser 165 170 175

His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr Tyr 180 180 185

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aac atc cag acc aag aac aaa gcc atc tcc tac atg gac tgc ctc aca 97

			<u> </u>						32								
Asn	Ile	Gln	Thr 20	Lys	Asn	Lys	Ala	11e 25	Ser	Tyr	Met	Asp	Cys 30	Leu	Thr		
											gac Asp						145
		_	_		-				_		tgc Cys 60						193
	_			_							ctc Leu						241
					_	_					cat His			_	_	•	289
_					_		-				cca Pro						337
_	_					_	_	-			gat Asp			_			385
_	_	_				_				_	ggc Gly 140						433
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80

Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys 100 105 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Arg Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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c tgg gtt gac atc tgt ttc agc act tgc atc atc ccc aag atg ctg gtg Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Ile Pro Lys Met Leu Val 1 5 10 15 aac atc cag acc aag aac aaa gcc atc tcc tac atg gac tgc ctc aca Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30 cag gtc tat ttc tcc atg ctt ttt cct att ctg gac acg cta ctc ctg Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc ctc cct ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His 50 55 60 tac atg atc atc atg aac ccc cgc ctc tgt ggc ctc ctg att ttt gtc Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80
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Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30 cag gtc tat ttc tcc atg ctt ttt cct att ctg gac acg cta ctc ctg Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc ctc cct ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His 50 55 60 tac atg atc atc atg aac ccc cgc ctc tgt ggc ctc ctg att ttt gtc Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80
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Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu Ass Thr Leu Leu Leu Ass Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His So Tar Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val As Romannia Romann
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tac atg atc atc atg aac ccc cgc ctc tgt ggc ctc ctg att ttt gtc Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80
Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80
Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val 65 70 75 80
65 70 75 80
atc tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg 289
Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95
·
atg cat cta atc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337
Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110
gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

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atg Met	tcc Ser	tca Ser	tct Ser	ggg Gly 165	gga Gly	aaa Lys	caa Gln	aaa Lys	gca Ala 170	ctt Leu	tcc Ser	acc Thr	tgt Cys	ggg Gly 175	tct Ser	529
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ttc Phe	act Thr	tct Ser 195	gca Ala	gtg Val	act Thr	cac His	gct Ala 200	tcc Ser	cag Gln	aaa Lys	atc Ile	tcc Ser 205	gtg Val	gcc Ala	tcg Ser	625
			acg Thr													649
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Gln	. Val	. Туг 35	Phe	. Ser	Met	Leu	Phe 40	Pro	Ile	. Leu	. Asp	Thr 45	Leu	. Leu	. Leu	
Thr	Va]	. Met	: Ala	Туг	: Asp	Arg 55	Phe	e Val	. Ala	lle	60	Leu	Pro	Leu	His	

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Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met 85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180 185 190

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tctgtcaccc tctatatcat tcagccatca tgaacccgtg tttctgtggc tttctagttg 240

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acetgetica aggatgigga aatteetaat tieetetigig aceettetea acteegeeat 360
etigeatgit gigacateit eaceaataac ataateatgi attiteetige tigeegiatit 420
gigiteette eeatetegig gaeeetitee tettaetata aaatgitte eteeatietig 480
aggetticat eigeaggigg gaagtataaa geetteteea eetigigigite teaeetigiea 540
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caa Gln																145
gca Ala																193
tac Tyr 65	aca Thr	gtt Val	gca Ala	atg Met	tcc Ser 70	cag Gln	agg Arg	ctt Leu	tgc Cys	tcc Ser 75	ttg Leu	ttg Leu	gtg Val	gct Ala	aca Thr 80	241
tca Ser	tac Tyr	tct Ser	tgg Trp	82 GJA āāā	ata Ile	gtc Val	tgt Cys	ttc Phe	ctg Leu 90	aca Thr	ctt Leu	acc Thr	tac Tyr	ttt Phe 95	cta Leu	289
ctg Leu	gaa Glu	tta Leu	tcc Ser 100	ttc Phe	aga Arg	gga Gly	aat Asn	aat Asn 105	atc Ile	att Ile	aat Asn	aac Asn	ttt Phe 110	gtc Val	tgt Cys	337
			gcc Ala													385
			act Thr													433
			ttc Phe													481
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			gcc Ala 180	Ile					Gly					Leu		577

tgt gtt cct aac tcc aaa agt tca tgg ctc atg gtc aag gtg acc tct 625 Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Thr Ser 200 205 195 649 gtc ttt tac aca gtg ttc att ccc Val Phe Tyr Thr Val Phe Ile Pro <210> 39 <211> 216 <212> PRT <213> Hylobates lar <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9580; gene = HLA74; Accession DDBJ/EMBL/GenBank = AF127840 Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu 5 Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met 25 20 Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu 40 35 Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu 50 Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr 75 65 Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu 85 Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys 105 100 Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser 120 115 Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu

135

130

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Asn	Ile	GIn	Thr 20	His	Asn	гàг	vaı	25 25	Thr	ıyr	Ala	GIŢ	Cys 30	TTE	THE	
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Gln	Met		Phe	Phe	Leu	Leu		Val	Gly	Leu	Asp		Phe	Leu	Leu	
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val 85 90 95

Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Cys
100 105 110

Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Gly Pro Leu 130 135 140

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	Phe Ser Thr	ggc act gag att Gly Thr Glu Ile 105	_	-
		gtg gcc tgc tct Val Ala Cys Ser 120		
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Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Ile Met Asn Ser Trp Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Ile Val Ser Ile Leu Cys Ser Pro Leu Gln Ser Ile Met Ala 85 90 95

Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His Phe Cys 100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Ile Lys 115 120 125

Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu 130 135 140 Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser 150 155 145 Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser 170 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr 185 Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser 200 Val Met Tyr Thr Val Val Thr Ser <210> 50 <211> 649 <212> DNA <213> Gorilla gorilla <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9593; gene = GGO3; Accession DDBJ/EMBL/GenBank = AF127848 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor <400> 50 49 c ttt gtg gac acc tct ttc atc tcc acc aca gtc ccc aag atg cta gtg Phe Val Asp Thr Ser Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val .10 97 aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr 25 145 cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu 193 gcc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55 241 tac acq qtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala 70 75

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Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met . 85 90 95

Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn 115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val 130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg 145 150 155 160

Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile 165 170 175

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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca	180
tctgtcaccc tctatatcat tcagccatca tgaacccgtg tttctgtggc ttcctagatt	240
tgctgtcttt tttttctttc tttttctcag tcttttagat ggtcagctgc agaacttgat	300
tgccttacaa atgacctgct tcgaggatgt gggaattcct aatttcctct gtgacccttc	360
tcaactgccc catctcacat gttgtgacat cttcaccaat cacataatca tgtatttccc	420
tgctgccata tttggttttc ttcccatctc ggggaccctt ctctcttacc atgtaattgt	480

ttcctccatt ctgagggttt catcatctat gggaggtgta aagccttccc cacctgtgag	540
ttgtttgctg atattatgga acaggcttcg gagggtacct cagttcagat gtgttatctt	600
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aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly 20 25 30	97
cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu 35 40 45	145
act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	193
tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly 65 70 75 80	241
tcc tgg tgc atc agt gtc atg ggt tcc ctg ctc gag acc ttg act gtt Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val 85 90 95	289
ttg agg ctg tcc ttc tgc acc aaa atg gaa att cca cac ttt ttt tgt Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys 100 105 110	337
gat ctt ctt gaa gtc ctg aag ctc gcc tgt tct gac acc ttc att aat Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn 115 120 125	385
aac gtg gtg ata tac ttt gca act ggc gtc ctg ggt gtg att ccc ttc Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe	433

									"								
	130					135					140						
act Thr 145	gga Gly	ata Ile	ttt Phe	ttc Phe	tct Ser 150	tac Tyr	tat Tyr	aaa Lys	att Ile	gtt Val 155	ttc Phe	tct Ser	ata Ile	ctg Leu	agg Arg 160	481	Ī
att Ile	tcc Ser	tca Ser	gct Ala	ggg Gly 165	aga Arg	aag Lys	cac His	aaa Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	529)
cac His	ctc Leu	tca Ser	gtg Val 180	gtc Val	acc Thr	ttg Leu	ttc Phe	tat Tyr 185	Gly	acg Thr	ggc Gly	ttt Phe	ggg Gly 190	gtc Val	tat Tyr	577	,
			gca Ala													625	5
			acc Thr	_												649)
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			Leu	Cys 5	Phe	Thr	Ser	Thr	Thr 10	Val	Pro	Lys	Met	Leu 15	Leu		
Asn	Ile	Leu	Thr 20	Gln	Asn	Lys	Phe	Ile 25	Thr	Tyr	Ala	Gly	Cys 30	Leu	Gly		
Gln	Ile	Phe 35	Phe	Phe	Thr	Ser	Phe 40	Gly	Cys	Leu	Asp	Asn 45	Leu	Leu	Leu		
Thr	Val 50	Met	Ala	Tyr	Asp	Arg 55	Phe	Val	Ala	Ile	Суз 60	His	Pro	Leu	His		
Тут 65	Thr	Val	Ile	Met	Asn 70	Pro	Arg	Leu	Суз	Gly 75	Leu	Leu	Val	Leu	Gly 80		
Ser	Trp	Cys	Ile	Ser	Val	Met	Gly	Ser	Leu	Leu	Glu	ጥከተ	Len	Thr	Va1		

Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Cys 110 The Cys 105 The Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn

Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe 130 135 140

120

Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Ala Ala Ser 195 200 205

Val Met Tyr Thr Met Val Thr Pro 210 215

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115

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<222> (2)..(649)

<223> Product = olfactory receptor

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1 5 10 15

aac atc cga aca cgg agt cag agc atc acg tat gca gcc tgc ctc acc

Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr

20
25
30

-	_	_		_	_					_	-			ctc Leu	_	145
		atg										cat		ctg Leu		193
		_		_			-		-			_		ctt Leu	_	241
	_			_		-	_		_			_	_	atg Met 95	_	289
_		_			-			_						ttc Phe	_	337
	_		Gln	_										atc Ile		385
		_				_	-			_			_	cct Pro	-	433
								-		_			_	ttg Leu	-	481
_	_		_	-		_			_				-	ggc Gly 175		529
		_	_			_						_		gtg Val		577
													Val	gct Ala		625
_	_		_	gtg Val	-											649

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<211> 216 <212> PRT

<213> Eulemur fulvus

<220>

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<223> Taxon = 13515; gene = EFU35; Accession DDBJ/EMBL/GenBank = AF127852

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Leu Thr Asp Ile Cys Leu Ser Thr Ala Thr Val Pro Lys Met Leu Ala 1 5 10 15

Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr 20 25 30

Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg 50 55 60

Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu 65 70 75 80

Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys 100 105 110

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn 115 120 125

Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu 130 135 140

Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Leu Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

Ile Ser Ser Ala Phe Met His Ser Pro Arg Thr Met Ala Val Ala Ser

205 195 200

Met Met Tyr Thr Val Val Thr Pro 210 .

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gcacagcaag gccatcacat acaaaggctg cctcacccag atgtgttttt tcttgatttt
                                                                    180
tggtgggcta gtttgctact gacggtgatg gcctatgacc ggttcgtggc catctgtcac
                                                                    240
cccctgcgct acatggtcat catgaacccc aggctctgtg gtcttctgct tctcctttct
                                                                    300
tggttgatct gcttgacgta ttctctgctg caaagtctga tggttttgag ggtgtccttc
tgccaagaaa tagaaatccc ccactacttc tgtgaacttg ctcagatcct cacgctcgcc
                                                                    360
tgctctgaca ccctagttaa tgacgtcctg ctgtattttc tatctgctct gctcggtgtt
                                                                     420
attcccctga ctgggatcct ttattcttat tccagaatta tctcctccat aatgtgcatt
                                                                     480
tectetgetg gagggaagta caaageettt tecacetgtg ggteteacet etcegtegte
                                                                     540
tccttgttct acggtacagg ccttggggtc tacctaactt ctgaaacagc ccagcctcc
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AF127854 <400> 59

<210> 59

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tcacagcaga gtcatctcct ctgggggctg tctgacccag atgtctcttg ctctgctttt

<210> 60 <211> 652 <212> DNA <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(652) <223> Taxon = 34829; gene = ERU38; pseudogene; Accession DDBJ/EMBL/GenBank = AF127855 <400> 60 ctttgttgac atctgtttca cctccaccac catccccaag atgctggtga acattgacac 60 acacagcaaa gacatctcct acgtgggatg cctcactcag atgtattttt tcatggtgtt 120 tggtggactg gacaacttcc tcctgaccgt gatggcctgt gaccggtttg tggccatctg 180 tcacccctg cactatgcag tacagtcatc atgaaccccc gcttctgtgc cctcctggtt 240 ctgatgtctt ggttcatcat gtccctggat gccctggttc atgttctact tatactgagg 300 ctgacctttt ccttagaaac tgaaatccca catttcttct gtgacctggc tcagatgctc 360 gaggtggccc gctctgacac ctttatcaat aacatctgct tgtacttgtt ggctgtgttg 420 ctgtatgttt cctgtcacgg ggatcctcta cccctactct aaaattgtct cctccttaat 480 gaggatgtcc tccactgcag gcaagaagaa agcattttcc acctgtgggt ctcacctctc 540 tgtggtcctc ttgttctatg gaacaggact tggggtctac ctaagttctg ctgtgacccc 600 652 ttetteccag ageagegeea ttgeeteagt gatgtacaca gtagteacee ce

<210> 61

<211> 648

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									02	٠.						
		35					40					45				
	-	g atg l Met	-		-									_		193
	r Me	g gtc t Val		_			_		_	_		_	-		_	241
	_	g ttc p Phe		_		-										289
		g ctg g Leu														337
_		g gct l Ala 115	Gln			-		_	-		_					385
		c tgc e Cys 0														433
	t Gl	g atc y Ile								_				_		481
	_	c tcc r Ser			-	_			-				_			529
		c tgt u Cys														577
		c tct r Ser 195	Ala					Ser	-	-	_		Ile	_		625
	-	g tac t Tyr 0	_		-									•		649
_,	210-	62														
	212>	PRT														
	213>		mur	rubr	iven	ter										
	220>		_													
Hit Ct Les St Ve	cc ageu Se cg at 210> 211> 212> 213>	c tctr Ser 195 g tac t Tyr 0 63 216 PRT	Val 180 gct Ala acg Thr	yal gtg val gtg val	acc Thr gtc Val	cct Pro acc Thr 215	tct Ser 200	Tyr 185 tcc Ser	Gly	Thr	Ala	gcc Ala	Gly 190 att Ile	Val gcc	Tyr tca	625

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Gln Val Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met 65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile 85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys 100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn 115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val 130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ala Ile Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

5

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WO 01/46262		65	PCT/IB00/02017
	Lys Val Ile S	tct tac aca ggc tgc atc Ser Tyr Thr Gly Cys Ile 25	
		gga ctg gac aac ttc ctc Gly Leu Asp Asn Phe Leu 45	
		gcc atc tgt cac ccc ctg Ala Ile Cys His Pro Leu 60	
		tgt gta ttt ctt gtt ctg Cys Val Phe Leu Val Leu 75	
		ttg tca caa agc tta atg Leu Ser Gln Ser Leu Met 90	
	Thr Asp Leu (gaa atc ccc cac ttt ttc Glu Ile Pro His Phe Phe 105 110	
		tgt tcg gac acc ttt ctt Cys Ser Asp Thr Phe Leu 125	
		ctg ctg ggt ggg gga tgc Leu Leu Gly Gly Gly Cys 140	
		ata gtt tcc tcc gta cgt Ile Val Ser Ser Val Arg 155	
	Lys Cys Lys	gca ttt tcc acc tgt gca Ala Phe Ser Thr Cys Ala 170	
	Leu Phe Tyr	tgt aca tgc cta ggg gtg Cys Thr Cys Leu Gly Val 185 190	
		tcc agc gca aca gcc tcg Ser Ser Ala Thr Ala Ser 205	
tac acg gtg gtc act Tyr Thr Val Val Thr			643

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<212> PRT

<213> Eulemur fulvus

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<223> Taxon = 13515; gene = EFU57; pseudogene; Accession DDBJ/EMBL/GenBank =

AF127859

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Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln 20 25 30

Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr 35 40 45

Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr 50 55 60

Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser 65 70 75 80

Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu 85 90 95

Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu 100 105 110

Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp 115 120 125

Val Val Met Tyr Leu Ala Val Met Leu Cly Cly Cly Cys Leu Thr 130 135 140

Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile 145 150 155 160

Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His 165 170 175

Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu

180 185 190

Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met 195 200 205

Tyr Thr Val Val Thr Pro 210

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                                                                    120
                                                                     180
tggacttctg gacaatctga tgctgatggt catggcttat gaccactttg tggccatctg
                                                                     240
teaccetetg cactacacag teatcatgaa cecagtgete tgtgtecagg tgettgteca
caccgggctt gtcagcatcc tgggggcctt cctcggagag tgaccgtgtt gcggcttctt
                                                                     300
ttggtgcagt cactgaaatc ccacactatt tctgtgagct ccctgaggct ctccagctct
                                                                     360
                                                                     420
cccactctga cccctccatc aataatgtca tattatacat tgtgacggtg tcatgggctt
ctttcctctt gctgagattc ttttctctta ttctccaact gttttttctg tcctgaggat
                                                                     480
ctcaacagca ggggggaagt ataaagtgtt ttcctcctgt gagtctcacc tctcggttgt
                                                                     540
                                                                     600
ctgcctgttc tgtgggacct gcctggggtc tagctcagtt ccacatggac acacgcttct
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<210> 68
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aat ttc ctg tca gag aca aag gcc atc tcc tat gtg ggc tgt ctg gtc Asn Phe Leu Ser Glu Thr Lys Ala Ile Ser Tyr Val Gly Cys Leu Val 20 25 30	97										
cag atg tac ttc ttc atg gcc ctt gca aac act gac agc tac cta ctg Gln Met Tyr Phe Phe Met Ala Leu Ala Asn Thr Asp Ser Tyr Leu Leu 35 40 45	145										
gcc tcc atg gct att gac cgg ctg gtg gcc atc tgc aaa ccc ttc cac Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Lys Pro Phe His 50 55 60	193										
tat gat gtg gtt atg agc cca cgg cgt tgc ctc ctc atg ctg ttg ggt Tyr Asp Val Val Met Ser Pro Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80	241										
tct tgc acc atc tcc cac cta cac tcc ctg ttc cgg gtg cta ctc atg Ser Cys Thr Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95	289										
tct cgc ctg tct ttc tgt gcc tcc cac atc att aag cac ttt ttc tgt Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys 100 105 110	337										
gat acc cag cct gtg cta aag ctt tcc tgc tct gac aca tcc tcc agc Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125	385										
cag att gtg gtc atg acc gag acc ctg gct gtc atc gtg acc ccc ttc Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140	433										
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atc ccc tct gca gcc ggg aag tgg aag gcc ttc tcc acc tgt ggc tcc Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175	529										
cac ctc act gtg gtg gtc ctg ttc tat ggc agt gtc atc tat gtg tat His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr 180 185 190	577										
ttc agg ccc ctg tcc atg tac tca gtg atg aag gac cgg gta gcc aca Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Asp Arg Val Ala Thr 195 200 205	625										

649 gtt atg tac acg gta gtg aca cct Val Met Tyr Thr Val Val Thr Pro <210> 69 <211> 216 <212> PRT <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 34829; gene = ERU67; Accession DDBJ/EMBL/GenBank = AF127861 Phe Met Asp Ile Cys Phe Thr Thr Val Ile Val Pro Lys Met Leu Val 5 Asn Phe Leu Ser Glu Thr Lys Ala Ile Ser Tyr Val Gly Cys Leu Val 25 . 30 . 20 Gln Met Tyr Phe Phe Met Ala Leu Ala Asn Thr Asp Ser Tyr Leu Leu 40 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Lys Pro Phe His 50 Tyr Asp Val Val Met Ser Pro Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 Ser Cys Thr Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95 Ser Arg Leu Ser Phe Cys Ala Ser His Ile Ile Lys His Phe Phe Cys 105 100 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser **12**5 115 120 Gln Ile Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140 Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Ala 150 155 160 145

Ile Pro Ser Ala Ala Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser 170 165 His Leu Thr Val Val Val Leu Phe Tyr Gly Ser Val Ile Tyr Val Tyr 185 180 Phe Arg Pro Leu Ser Met Tyr Ser Val Met Lys Asp Arg Val Ala Thr 200 Val Met Tyr Thr Val Val Thr Pro 210 <210> 70 <211> 649 <212> DNA <213> Eulemur fulvus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 13515; gene = EFU83; Accession DDBJ/EMBL/GenBank = AF127862 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor c ttt tct gac atc tgc ttg gtc tcg acc act gtc cca cag atg ctg gtg 49 Phe Ser Asp Ile Cys Leu Val Ser Thr Thr Val Pro Gln Met Leu Val 10 97 aat gtg cag aca cac agc aaa gtc ata tcc tac gca ggc tgc gtc acc Asn Val Gln Thr His Ser Lys Val Ile Ser Tyr Ala Gly Cys Val Thr 25 30 20 cag atg gac ttc ttt gta ctc ttt gta ggg ctg gac agc ttc ctc ctt 145 Gln Met Asp Phe Phe Val Leu Phe Val Gly Leu Asp Ser Phe Leu Leu 35 acc gtg atg gcc tat gac cgg ttt gtg gtc atc tgc cac cca ctg cac 193 Thr Val Met Ala Tyr Asp Arg Phe Val Val Ile Cys His Pro Leu His 50 tac gcg gtc acc atg aac ccc agg ctc tgt ggg ctg ctg gtg ctg ctg 241 Tyr Ala Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Leu 70 65 289 tct tgg atc atg agt gcc ctg agt tcc ttg tta gaa agc tta gtg gtg

Ser Trp Ile Met Ser Ala Leu Ser Ser Leu Leu Glu Ser Leu Val Val

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gaa Glu	ctt Leu	aat Asn 115	gag Glu	ata Ile	atc Ile	cac His	ctg Leu 120	gcc Ala	tgt Cys	tct Ser	gac Asp	acc Thr 125	ttt Phe	ctt Leu	att Ile		385
	atg Met 130																433
gct Ala 145	Gly	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	gta Val	cgt Arg	gca Ala 160		481
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Thr Val Met Ala Tyr Asp Arg Phe Val Val Ile Cys His Pro Leu His

55

Tyr Ala Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Leu 65 70 75

Ser Trp Ile Met Ser Ala Leu Ser Ser Leu Leu Glu Ser Leu Val Val 90

Leu Trp Val Cys Phe Cys Leu Asp Leu Glu Ile Pro His Phe Phe Cys 100 105

Glu Leu Asn Glu Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Ile 120 . 125

Asp Met Val Met Tyr Phe Ser Ala Leu Leu Leu Gly Gly Ser Leu 130 135

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr 185 190

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	cctggatcat	aagtggcccg	aattccttgt	tacaaagtgt	aaaggtgctg	tggctgtcct	300
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	tcctcttgct	gggatccttt	actcttactc	tcagatagtt	tcctccacac	gtgcactctc	480
	ctcagctcag	gcgaagtgta	aagcattttc	cacctgtgca	gctcacctcg	cggttgtctc	540
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aac att gaa aca cac agc aaa gac atc tcc tac atg gga tgc ctc act	97										
Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr											
20 25 30											
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Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu											
35 40 45											
3-5 3 3 3	193										
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His											
50 55 60											
	241										
Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile											
65 70 75 80											
	200										
500 055 000 mos mos mos mos gara gara and gara and gara and gara	289										
Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile											
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Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Cys	331										
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100 105 110											
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Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn	505										
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Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val											
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Met	Ser	Ser	Thr	Ala 165	Gly	Lys	Lys	Lys	Ala 170	Phe	Ser	Thr	Cys	Gly 175	Ser	
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			180					185					190			
ctc Leu	agt Ser	tct Ser	gct Ala	gtg Val	acc Thr	cct Pro	tct Ser	tcc Ser	cag Gln	agc Ser	agc Ser	Ser	att Ile	gcc Ala	tca Ser	625
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	atg Met		_			Thr										649
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1	· Val		Thr	5	•			Ile	10				Cys	15		
1				5	•				10					15		
1 Asn		Glu	Thr 20	5 His	Ser	Lys	Asp	Ile 25	10 Ser	Tyr	Met	Gly	Cys 30	15 Leu	Thr	
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Asn Glr	Ile Met	Glu Tyr 35	Thr 20 Phe	His Phe	Ser Met	Lys Ile Arg	Asp Phe 40	Ile 25 Ala Val	Ser Gly	Tyr Leu	Met Asp Cys	Gly Asn 45	Cys 30 Phe	Leu Leu	Thr Leu His	
Asn Glr Thr Tyr 65	a Ile a Met Thr	Glu Tyr 35	Thr 20 Phe Ala	His Phe Tyr	Ser Met Asp	Lys Ile Arg 55	Phe 40	Ile 25 Ala Val	Ser Gly Ala	Tyr Leu Ile Ala	Met Asp Cys 60	Gly Asn 45 His	Cys 30 Phe Pro	Leu Leu Leu	Thr Leu His	
Asn Glr Thr Tyr 65	Met Wal	Glu Tyr 35	Thr 20 Phe Ala	His Phe Tyr	Ser Met Asp	Lys Ile Arg 55	Phe 40	Ile 25 Ala Val	Ser Gly Ala	Tyr Leu Ile Ala	Met Asp Cys 60	Gly Asn 45 His	Cys 30 Phe Pro	Leu Leu Leu	Thr Leu His	
Asn Glr Thr 55	a Ile a Met Thr	Glu Tyr 35 Met	Thr 20 Phe Ala	His Phe Tyr	Ser Met Asp Ser 70	Lys Ile Arg 55 Pro	Phe 40 Phe Arg	Ile 25 Ala Val	Ser Gly Ala Cys	Tyr Leu Ile Ala 75	Asp Cys 60	Asn 45	Cys 30 Phe Pro	Leu Leu Leu Leu Leu 95	Thr Leu His Ile 80	

Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn 120 Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg 150 Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser 170 His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr 180 Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser 200 195 Val Met Phe Thr Val Val Thr Pro 210 <210> 76 <211> '646 <212> DNA <213> Macaca sylvanus <220> <221> misc_feature <222> (1)..(646) <223> Taxon = 9546; gene = MSY1; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127866 <400> 76 ctttgttgac atctgtttta tctccaccac cgtccccagg atgctgatga acatccaggc 60 atggagcaaa gacatctcct acgtggggtg cctcactcag gtgtattttt taatgatgtt 180 tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg ccacccctg cactacacgg tcatcatgaa cccctgcctc tgtggcctcc tggttctggc 240 atcttgattc atcattttat gggtctccct agttcatatt ctactgatga agagtttgat 300 360 ctccataggc actgagattc cgcatttctt ctgtgaactg gctcaggtcc tcaaggtggc

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gcttcctgta gctgggatcc tcttctccta ctctcagatc gtctcctcct taatgaggat

420

480

	- 40
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acc gtg atg gcc tac gac agg ttt gtg gcc atc tgt cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	193
tac acg gtc acc atg aac ccc agg ctc tgt gga ctg ctg gtt ctg gcg Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80	241
tcc tgg atc atg agt gcc ctg aat tct tca ttg caa agc tta atg gta Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val 85 90 95	289
ttg cac ctt tcc ttc tgt gca gac ttg gaa att ccc cac ttt ttc tgt Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110	337
gaa ctt aat cag gtc atc cac ctt acc tgt tct gac act ttt ctt aat Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn 115 120 125	385
gac atg gtg atg tat ttg tca gct gtg ctg ctg ggt ggg gga tgt ctc	433

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I.	tt le 45	ggg ggg	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	atc Ile	gtc Val 155	tcc Ser	tct Ser	ata Ile	cat His	gca Ala 160	,	481
a:	tc le	tca Ser	tca Ser	gtt Val	cag Gln 165	Gly ggg	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser	!	529
							tta Leu											577
C L	tt eu	agt Ser	tct Ser 195	gct Ala	gca Ala	acc Thr	cac His	agc Ser 200	tca Ser	cac His	gca Ala	agt Ser	gct Ala 205	gca Ala	gtc Val	tcg Ser		625
-	_	_				_	acc Thr 215											649
< < < < <	220 220 220	1> : 2> : 3> : 0> : 1> : 2> :	misc	ca s _fea .(64	ture 9)			MOV	12.).	agio	תת ת	D.T / F	MDT./	ConR	ank -	a r. 1 2	7867
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1					5					10					15			
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G	Sln	Met	Cys 35	Phe	Phe	lle	Phe	Phe 40	Ala	Gly	Leu	qaA .	Ile 45	Phe	Met	Leu		
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	_	_			-										. 160+	17-1		

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val

85 90 95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu 130 140

Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala 145 150 155 160

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

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aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc 97
Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser

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	gcc tat gac cgg t Ala Tyr Asp Arg T 55	Tyr Val Ala Ile		
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	ctc agc ttg tca t Leu Ser Leu Ser T 85			
	tcc ttt tgc acc a Ser Phe Cys Thr S 100		-	_
	cag gcc ctc acg c Gln Ala Leu Thr I 1			
	ctc tac gtg gtg a Leu Tyr Val Val T 135			
	ctt ttc tcc tac a Leu Phe Ser Tyr T 150	-		
	aca gat ggg aaa c Thr Asp Gly Lys F 165	_		
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Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 50 . 55 60 .

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met 90 . 95

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys 105 100

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn 120

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe 135 140

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg 155

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser 165 170

His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 185 180

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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<221> misc_feature
<222> (1)..(647)
<223> Taxon = 9546; gene = MSY2; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127869
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                                                                    120
tgcaggattg gacaccttta tgctgaccgt gatggcctac gacaggtttg tggccatctg
                                                                    180
                                                                    240
tcaccctctg cactacacgg tcaccatgaa ccccaggetc tgtggactgc tggttctggc
gtcctgatca tgagtgccct gaattcttca ttgcaaagct taatggtatt gcacctttcc
                                                                    300
ttctgtgcag acttggaaat tccccacttt ttctgtgaac ttaatcaggt catccacctt
                                                                    360
acctgttctg acacttttct taatgacatg gtgatgtatt tgtcagctgt gctgctgggt
                                                                   420
gggggatgtc tcattgggat cctttactct tactctaaga tcgtctcctc tatacttgca
                                                                    480
atctcatcag ttcaggggaa gtacaaggca ttttccacct gtgcatctca cctctcggtt
                                                                    540
gtctccttat ttattgtaca atcctaggtg tgtaccttag ttctgctgca acccacagct
                                                                     600
                                                                    647
cacacgcaag tgctgcagtc tcggtgatgt acactgtggt taccccc
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<210> 82
<211> 649
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<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 82

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	aac Asn	atc Ile	cag Gln	aca Thr 20	cag Gln	agc Ser	aga Arg	gtc Val	atc Ile 25	acc Thr	tat Tyr	gca Ala	ggc	tgc Cys 30	atc Ile	acc Thr	97
	cag Gln	atg Met	tgc Cys 35	ttt Phe	ttc Phe	ata Ile	ttc Phe	ttt Phe 40	gtg Val	gga Gly	ctg Leu	gat Asp	atc Ile 45	ttt Phe	atg Met	ctg Leu	145
	Thr	gtg Val 50	atg Met	gcc Ala	ttt Phe	gac Asp	cgg Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	193
						aac Asn 70											241
						gcc Ala											289
						tgc Cys										tgt Cys	337
						gtc Val											385
						ttg Leu											433
						tct Ser 150											481
	Ile	Ser	Ser	Ala	Gln 165	Gly	Lys	Tyr	Arg	Ala 170	Phe	Ser	Thr	Cys	Ala 175	Ser	529
						tcc Ser				Gly					Val		577
				Ala		acc Thr			Ser					Ala			625
	gtg Val	atg Met	tac Tyr	acc Thr	gtg Val	gtt Val	acc Thr	Pro	:								649

210 215

<210> 83

<211> 216

<212> PRT

<213> Macaca sylvanus

<220>

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<222> (1)..(649)

<223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870

<400> 83

Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Met Val 1 5 10 15

Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr 20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Val Gly Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys 100 105 110 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly 145 150 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185 180 Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser 200 Val Met Tyr Thr Val Val Thr Pro <210> 84 <211> 646 <212> DNA <213> Macaca sylvanus <220> <221> misc_feature <222> (1)..(646) <223> Taxon = 9546; gene = MSY6; Accession DDBJ/EMBL/GenBank = AF127871 <220> <221> CDS <222> (2)..(646) <223> Product = olfactory receptor c ttc act gac ctc ttc ttt gtc acc aac aca atc ccc aag atg ctg gtg 49 Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val 10 aac ctc cag tcc cag aac aaa gcc atc tcc tat gca ggg tgt ctg aca 97 Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr 25 145 cag ctc tac ttc ctg gtc tcc ttg gtg gcc ctg gac aac ctc atc ctg Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu 193 get gtg atg geg tat gac ege tat gtg gee ate tge tge eee etc cac Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His tac acc aca gcc atg agc cct aag ctc tgt atc tta ctc ctt tcc ttg 241 Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ser Leu

acc acg gtg acc ttc tgt ggg tca cga aaa atc cac tac atc ttc tgt

Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys

100 105 110

90

tgt tgg gtc tta tct gtg ctc tat ggc ctc ata cac acc ttc ctc atg Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met 289

gag atg t Glu Met T													385
cac aca g His Thr V 130													433
gga ttc a Gly Phe M 145		Ile S											481
ata ccc t Ile Pro S													529
cat ttg g His Leu G													577
ctg aag c Leu Lys P 1													625
atg tat g Met Tyr A 210													646
	.5	ylvanu	· s										
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Asn Leu G	31n Ser 20	Gln A	sn Lys	Ala	Ile 25	Ser	Tyr	Ala	Gly	Суs 30	Leu	Thr	
Gln Leu 1	Tyr Phe 35	Leu V	al Ser	Leu 40	Val	Ala	Leu	Asp	Asn 45	Leu	Ile	Leu	

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His 50 55 60

Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ser Leu 65 70 75 80

Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met 85 90 95

Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys 100 105 110

Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn 115 120 125

His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe 130 135 140

Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg 145 150 155 160

Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr 180 185 190

Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val Ala Thr Val 195 200 205

Met Tyr Ala Val Val Thr Pro 210 215

<210> 86

<211> 649

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 86

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aac atc cag acc aag aac aaa acc atc tct tac atg gac tgc ctc acc Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30	97												
cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg cta ctc ctg Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45	145												
acc gtg atg gct tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50 55 60	193												
tat gta acc atc atg aac ccc cgc ctc tgc ggc ctc ctg gtt ttt gtc Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80	241												
acg tgg ctc att ggt gtc atg aca ccc ctc ctc cat att tct ctg ttg Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu 85 90 95	289												
acg cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys 100 105 110	337												
gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125	385												
agc acg ttg ata tat gtt atg aca ggt gtg ctg ggc gtt ttt ccc ctc Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140	433												
ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys 145 150 155 160	481												
atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175	529												
cac ctc tcc atc gtt tct tta ttt tat ggg aca ggc att ggg gtc cat His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His 180 185 190	577												
ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205	625												
gtg atg tac acg gtg gtt acc ccc Val Met Tyr Thr Val Val Thr Pro	649												

210 215

<210> 87

<211> 216

<212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872

<400> 87

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Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr 20 25 30

Gln Val Tyr Phe Ser Met. Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His 50 55 60

Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val 65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu 85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Cys 100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu 130 135 140

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 88 <211> 645 <212> DNA <213> Macaca sylvanus <220> <221> misc_feature <222> (1)..(645) <223> Taxon = 9546; gene = MSY8; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127873 <400> 88 ctttgttgac atctgtttta tctccaccac cgtccccagg atgctgatga acatccaggc 60 atggagcaaa gacatctcct acgtggggtg cctcactcag gtgtattttt taatgatgtt 120 180 tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg ccacccctg cactacacgg tcatcatgaa cccctgcctc tgtggcatcc tggttctggc 240 atcttgattc atcattttat gggtctccct agttcatatt ctactgatga agagtttgat 300 360 ctccataggc actgagattc cgcatttctt ctgtgaactg gctcaggtcc tcaaggtgcc 420 cgctctgata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg 480 cttcctgtag ctgggatcct cttctcctac tctcagatcg tctcctcctt aatgaggatg 540 tcctccaccg agggcaagta caaagccttt tccacctgtg ggtctcacct ctgtgtggtc teettattet atggaacagg acttggggte tateteagtt etgetgtgae ceattettee 600 cagagcagct ccatggcctc agtgatgtac accatggtca ccccc 645

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<210> 89
<211> 649
<212> DNA
<213> Macaca sylvanus
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<222> (1)..(649)
<223> Taxon = 9546; gene = MSY9; Accession DDBJ/EMBL/GenBank = AF127874
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<221> CDS
<222> (2)..(649)
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aac at Asn Il															97
cag at Gln Me	_														145
acc gt Thr Va	al Met														193
tac co Tyr Pr 65															241
tcc to Ser Tr			_	-				_		_	_	_	_	_	289
ctg ca Leu Gl															337
gag ct Glu Le	_	Gln	_		_		_	-							385
tac at Tyr II															433
	ga atc ly Ile								-				_	_	481
	ca tcc er Ser		_					-				-			529
	tg tct eu Ser		_										-		577
	gt tcc er Ser 195	Asn	-	_							_				625

gtc atg tac act gtg gtc acc ccc Val Met Tyr Thr Val Val Thr Pro 210

649

<210> 90

<211> 216

<212> PRT

<213> Macaca sylvanus

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<222> (1)..(649)
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Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val 5 10

Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu 35

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 55

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met 85 90

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys 105 100

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn 120

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe 130 135

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg 150 155

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 175 170 165 His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 185 Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser 200 Val Met Tyr Thr Val Val Thr Pro 210 <210> 91 <211> 649 <212> DNA <213> Callithrix jacchus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9483; gene = CJA21; Accession DDBJ/EMBL/GenBank = AF127875 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor <400> 91 c ttt gtg gac atc tgt gtt acc tcc acc aca ctt ccg aag aca ctg tca Phe Val Asp Ile Cys Val Thr Ser Thr Thr Leu Pro Lys Thr Leu Ser 10 97 aac atc cag aca cac agc aaa gtc atc acc tat gca ggc tgc gtc acc Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr 25 145 cag ttg tac ttc ttt gta ctc ttc ata ggg ttg gac agc tta ctc ccg Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55

tcc tgg atc atg agt gcc ctg cat tct ttg aca gaa agc tta atg gta

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val

85 90 95

tac cca ctg ctc ttt tgt aca gac ttg aaa atc ccc cag ttt ttc tgt 337

241

tac acg gtc atc atg aac cct cag ttc tgt gga ctg ctg gtt ctg gtg

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val

70

110 01/40202	•		94	}			
Tyr Pro Leu	Leu Phe Cys 100	Thr Asp	Leu Lys 105	Ile Pro	Gln Phe 110	Phe Cys	
gaa att cat Glu Ile His 115	-			_			385
aac ctg gtg Asn Leu Val 130	-				-		433
gct ggg atc Ala Gly Ile 145	-	Tyr Ser	_	_			481
atc tca tca Ile Ser Ser		_			-		529
cac ctc tca His Leu Ser			_				577
ctg agt tct Leu Ser Ser 195		_					625
gtg atg tac Val Met Tyr 210							649
<220>	thrix jacch	ius					
<222> (1)		ene = CJA	21; Acce	ssion DD	BJ/EMBL/O	GenBank =	AF127875
Phe Val Asp 1	Ile Cys Val	Thr Ser	Thr Thr 10	Leu Pro	Lys Thr	Leu Ser 15	
Asn Ile Gln	Thr His Ser 20	: Lys Val	Ile Thr 25	Tyr Ala	Gly Cys 30	Val Thr	
Gln Leu Tyr 35	Phe Phe Va	Leu Phe 40	Ile Gly	Leu Asp	Ser Leu 45	Leu Pro	

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

50 55 60

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val 85 90 95

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys 100 105 110

Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Gly Pro Leu 130 135 140

Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr His Ser Ser Leu Ser Ser Ala Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro · 210 215

<210> 93

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

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<222> (1)..(649)

<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876

<220>

<221> CDS

<222> (2)..(649)

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<223> Product = olfactory receptor																
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aac Asn						ggt Gly										97
						gtt Val										145
		_	_			cgg Arg 55										193
						ccc Pro										241
						tca Ser										289
						acc Thr										337
						acg Thr										385
		_			_	gtg Val 135		-								433
						tac Tyr										481
						aaa Lys										529
	_			_		tta Leu								-		577
	_		Asn	_	_	tcc Ser						_		-		625

gcc atg tac aca gtg gtc acc cct
Ala Met Tyr Thr Val Val Thr Pro
210 215

649

<210> 94

<211> 216

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876

<400> 94

Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Ile Leu Val 1 5 10 15

Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala 20 25 30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser 50 55

Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys 100 105 110

Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn 115 120 125

Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe 130 140

Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160 Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Trp Gly Met Val Ala Ser 195 200 205

Ala Met Tyr Thr Val Val Thr Pro 210 215

<210	> 9	95														
<211	> (549														
<212	> I	ONA														
<213	> (Calli	thri	х ја	cchu	ıs										
<220	>															
<221	> 1	nisc_	feat	ure												
<222	>	(1)	(649)												
<223	> 1	Faxor	1 = 9	483;	ger	e =	CJA2	23; A	cces	sion	1 DDE	J/EN	BL/C	enBa	ink = AF1	.27877
<220	>															
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<222	>	(2)	(649)												
<223	> 1	Produ	ict =	olf	acto	ry r	ecer	otor								
<400	> 9	95														
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Ph	e T	nr As	sp Il	.e C <u>}</u>	s Ph	ie Th	ır Th	ur Va	al II	le Va	al Pi	o Aı	g Me	et Le	eu Val	
1				5					10)				15	5	
															•	
aat	ttt	cta	tca	ggg	aca	aag	gtt	atc	ccc	tac	atg	ggc	tgc	ctg	gtc	97
Asn	Phe	Leu	Ser	Gly	Thr	Lys	Val	Ile	Pro	Tyr	Met	Gly	Cys	Leu	Val	
			20					25					30			
caa	atg	tac	ttc	ttc	atg	gcc	ttt	ggg	aac	act	gac	agc	tac	ctg	ctg	145
Gln	Met	Tyr	Phe	Phe	Met	Ala	Phe	Gly	Asn	Thr	Asp	Ser	Tyr	Leu	Leu	
		35					40					45				
gcc	tct	atg	gcc	atc	gac	cgg	ctg	gtg	gcc	atc	tgc	aac	CCC	tta	cac	193
Ala	Ser	Met	Ala	Ile	Asp	Arg	Leu	Val	Ala	Ile	Cys	Asn	Pro	Leu	His	
	50					55					60					
tat	gat	gtg	gct	atg	aac	CCC	cgg	cat	tgc	cta	ctc	atg	cta	ttg	ggt	241
Tyr	Asp	Val	Ala	Met	Asn	Pro	Arg	His	Cys	Leu	Leu	Met	Leu	Leu	Gly	
65	_				70		_			75					80	
tct	tgc	agc	atc	tcc	cac	cta	cat	tcc	ctg	ttc	cgg	gtg	cta	ctt	atg	289
			Ile													
	_			85					90	•	-			95		
tct	cac	ctg	tct	ttc	tgt	gcc	tcc	cac	gtc	att	aag	cac	ttt	ttc	tgt	337

•									99							
Ser	His	Leu	Ser 100	Phe	Cys	Ala	Ser	His 105	Val	Ile	Lys	His	Phe 110	Phe	Cys	
				gtg Val												385
cag Gln	atg Met 130	gtg Val	gtc Val	atg Met	act Thr	gag Glu 135	act Thr	tta Leu	gct Ala	gtc Val	att Ile 140	gtg Val	acc Thr	ccc Pro	ttc Phe	433
ctg Leu 145	tgt Cys	atc Ile	atc Ile	ttc Phe	tcc Ser 150	tac Tyr	ctg Leu	cga Arg	atc Ile	atc Ile 155	atc Ile	act Thr	gtg Val	ctc Leu	aga Arg 160	481
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				gta Val											tat Tyr	. 577
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Asn	Phe	Leu	Ser 20	Gly	Thr	Lys	Val	11e 25	Pro	Tyr	Met	Gly	Cys 30	Leu	Val	
Gln	Met	Tyr 35	Phe	Phe	Met	Ala	Phe 40	Gly	Asn	Thr	Asp	Ser 45	Tyr	Leu	Leu	•

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His

50 55 60

Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Leu Gly 65 70 75 80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95

Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Cys 100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160

Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr 180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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			cat His													145
			gcc Ala													193
	Thr	-	acc Thr				-	_	_				_			241
			ctg Leu													289
_			tcc Ser 100		_		_	_	_							337
_			cag Gln	-												385
_			atg Met		_	-	-									433
_	Gly	Ile	ctt Leu	Tyr	Ser	Tyr	Ser	Lys	Ile	Val	Ser					481
			gct Ala													529
			att Ile 180													577
	_		gct Ala	_				Ser			-	_	_	_	_	625

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649

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<400> 98

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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25

Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 75 70 65

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 85 90

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Pro Leu 135 140 130

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 160 145 150 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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Ph	e Ā	la Ās	p II	e Cy	s Pr	ne Tî	ır Se	er Th	ır Th	ır Va	al Pr	o Ly	ys Me	et Le	eu Val	
1			-	5					10					15		
											•					
gat	atc	caa	aca	caa	agc	aaa	atg	atc	act	ttt	gca	ggg	tgc	ctc	acc	97
Asp	Ile	Gln	Thr	Gln	Ser	Lys	Met	Ile	Thr	Phe	Ala	Gly	Cys	Leu	Thr	
			20			-		25					30			
cag	att	ttt	ttt	ttc	att	gca	ttt	gga	tgc	ctg	gac	aat	ttg	ctc	ttg	145
		Phe														
		35					40	_	-		_	45				
acc	ata	atg	acc	tat	gac	caa	ttc	ata	acc	atc	tat	cac	ccc	ctg	cac	193
Thr	Val	Met	Ala	Tvr	Asp	Ara	Phe	Val	Ala	Ile	Cvs	His	Pro	Leu	His	
	50			-1-		55					60					
	-															
tac	acc	gtc	atc	ato	aac	CCC	caa	ata	tat	aga	cta	cta	att	cta	aga	241
		. Val														
65	ATC	· vai	110	1100	70		•9	200	٠, ٥	75					80	
0.5					, ,											
taa		, tgc	240	art	a+ a	2+4	~++	tot	cta	ctc	gag	acc	tta	acc	att	289
		Cys														
ser	LIT	CAR	тте	85	val	met	val	Ser	90	Lea	314	1114	DÇU	95		
				65					30					,,		
A. A			.						~~~		aa^			+++	tat	337
ttg	agg	, ctg	tcc	CCC	tgc	aca	aac	atg	gaa	atc	cca	cac	CCE	LLE	cgt	,,,

	,							104	+							
Leu Arg		Ser 100	Phe	Cys	Thr	Asn	Met 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys		
gat gtt Asp Val															385	
aaa atc Lys Ile 130															433	
tct gga Ser Gly 145															481	
gta tca Val Ser		_						-							529	
cac ctc His Leu	Ser														577	
ctc agt Leu Ser															625	
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Gln Ile	Phe 35	Phe	Phe	Val	Ala	Phe 40	Gly	Cys	Leu	Asp	Asn 45	Leu	Leu	Leu		

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

50 55 60

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 115 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 145 150 155 160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr 180 185 190

Leu Ser Leu Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser 195 200 205

Val Met Tyr Thr Met Val Thr Pro 210 215

<210> 101

<211> 649

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gtg atg tac aca gtg gtc act ccc 649

PCT/IB00/02017

gtg atg tac aca gtg gtc act ccc Val Met Tyr Thr Val Val Thr Pro 210 215

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Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30

Gln Met Ser Phe Ser Ile Phe Phe Val Cys Met Glu Asp Met Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Pro Val Ile Met Ser Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80

Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95

Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn 115 120 125

Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro 130 135 140

Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu 145 150 155 160

Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser 165 170 175

Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val 180 185 190

Tyr Leu Gly Ser Ser Val Ser Ser Pro Arg Lys Arg Val Val Thr Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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Ph	e Va	l As	p Il	е Су	s Ph	e Va	l Se	r Th			l Pr	о Гу	s Th		u Val	
1				5					10					. 15	•	
																97
aat	atc	cag	aca	cac	agc	aaa	gtc	atc	acc	ttt	gca	ggc	tgc	atc	acc	91
Asn	Ile	Gln		His	Ser	Lys	Val		Thr	Pne	Ата	GLY		тте	Tur	
			20					25					30			
															ata	145
cag	ata	ggc	cat	tgc	CTC	CEC	משם	gca	gca	ttg	gac	guu	Dha	Mot	Lou	147
Gln	IIe		His	Cys	Leu	ьеи		Ата	vaı	гел	ASD	45	Pne	Mec	рец	
		35					40					43				
														ata	Cac	193
act	gtg	atg	gcc	tat	gac	cgg	Cat	gtg	31-	atc	Cyc.	ude	Dwa	Lou	uic vic	173
Thr		Met	Ala	тут	Asp		TYL	var	Ald	Ile	60	urs	FIG	Deu	1113	
	50					55					00					
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										gga Gly						
_	Thr	vaı	Thr	тте	70	PIO	Arg	neu	Cys	75	пеп	Deu	Vai	пеа	80	
65					70					15					00	
h				-a+	~~~	at-~	22±	+00	tos	tta	cae	acc	tta	ata	ata	289
										Leu						
ser	rrp	тте	neg	85	нта	שמש	ven	Ser	90	nea	3111	* 117	neu	95	T VA.	
				00					50					,,		

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337

Leu	Arg	Leu	Ser 100	Phe	Суѕ	Thr	Asp	Leu 105	Glu	Ile	Pro	His	Phe 110	Phe	Cys	
_			_	gtc Val				_	_		_					385
_			-	tat Tyr	_	_	_		_	-						433
_				tac Tyr				_		_				-	gca Ala 160	481
				cag Gln 165												529
				gtc Val											tac Tyr	577
															A	CO.

ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg 625 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser 200 195

649 gtg atg tac act gtg gtc acc ccc Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 104

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<212> PRT

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Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25

Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu 35 40

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His

60

50

55

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn 115 120 125

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 150 155

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 105

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<212> DNA

<213> Callithrix jacchus

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<222> (1)..(649)

<223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882

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			tca Ser 20														97
			ttc Phe													:	145
			gcc Ala							Ile						;	
tat Tyr 65	gat Asp	gtg Val	gct Ala	atg Met	aac Asn 70	tcc Ser	cgg Arg	cgt Arg	tgc Cys	cta Leu 75	ctc Leu	atg Met	cta Leu	ttg Leu	ggt Gly 80	:	241
			atc Ile														289
			tct Ser 100														337
			cct Pro														385
			gtc Val														433
			atc Ile														481
atc Ile	ccc Pro	tct Ser	gca Ala	gcc Ala 165	Gly	aag Lys	tgg Trp	agg Arg	gcc Ala 170	Phe	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tcc Ser		529
			gta Val 180														577
			ctg Leu					Val					Val				625

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gtt atg tac aca gta gtg aca ccc Val Met Tyr Thr Val Val Thr Pro 210 215 649

<210> 106

<211> 216

<212> PRT

<213> Callithrix jacchus

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<222> (1)..(649)

<223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882

<400> 106

Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val

Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val 20 25 30

Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu 35 40 45

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His 50 55 60

Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly 65 70 75 80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met 85 90 95

Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys 100 105 110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser 115 120 125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe 130 135 140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg 145 150 155 160 WO 01/46262 PCT/IB00/02017

Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr 180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210>	107			•											
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<221>	misc_	feat	ure												
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Phe	Ala As	sp Il	e Cy	rs Ph	e Th	ır Se	er Th	ır Th	ır Va	ıl Pr	o Ly	s Me	et Le	u Val	
1		_	5					10					15		
gat at	c caa	aca	caa	agc	aaa	atg	atc	act	ttt	gca	ggg	tgc	ctc	acc	97
Asp Il	e Gln	Thr	Gln	Ser	Lys	Met	Ile	Thr	Phe	Ala	Gly	Суѕ	Leu	Thr	
.		20			_		25					30			
cag at	t ttt	ttt	ttc	gtt	gca	ttt	gga	tgc	ctg	gac	aat	ttg	ctc	ttg	145
Gln Il	e Phe	Phe	Phe	Val	Ala	Phe	Gly	Cys	Leu	Asp	Asn	Leu	Leu	Leu	
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acc gt	σ atσ	acc	tat	σac	caa	ttc	ata	qcc	atc	tgt	cac	ccc	ctg	cac	193
Thr Va	1 Met	Ala	Tyr	Asp	Ara	Phe	Val	Ala	Ile	Cvs	His	Pro	Leu	His	
50			-3-		55					60					
					-										ŧ
tac go	a atc	atc	ato	aac	ccc	caa	ata	tat.	aga	cta	cta	att	cta	aaa	241
Tyr Al															
65	.a var		1100	70				0,70	75					80	
05				, 0											
tee te	-~ +~~	2+0	~~+	at a	atr	~++	tot	cta	ctc	gag	acc	tta	acc	att	289
Ser Tr	g tyc	TIO	com	37-1	Mot	Ual	Cor	Leu	Len	Glu	Thr	Len	Thr	Tle	
ser Ti	р сув	тте		val	Mec	Val	Ser	90	пец	GIU	1111	Dea	95	110	
			85					30					,,		
		.		.					250	-	~~	+++	+++	tat	337
ttg ag	g ctg	TCC	ttc	cgc	aca	aac	acg	gaa	alc	cca	Cac		LLL	LyL	JJ 1

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
100 105 110

gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn

115 120 125

aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc 433

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu

130 135 140

tot gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg

145 150 155 160

gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct
Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His

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Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly 65 70 75 80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn 115 120 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg 145 150 155 160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

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WO 01/46262 PCT/IB00/02017

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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

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Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys 100 105 110

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Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu 130 135 140

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tac cca gtt a Tyr Pro Val 5	acc atg aac Thr Met Asn 70	cca tgt ttc Pro Cys Phe	tgt ggc ttc Cys Gly Phe 75	cta gtt ttg Leu Val Leu	ttg 241 Leu 80
tct ttt ttt c Ser Phe Phe I					
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				acc ttc acc Thr Phe Thr 125	
				ttt ctt ccc Phe Leu Pro	
		Tyr Tyr Lys		tcc att ctg Ser Ile Leu	
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Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu 65 70 75 80

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Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile 130 . 140

PCT/IB00/02017 WO 01/46262 121

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654

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Phe	Val As	sp Th	ır Cy	s Pi	ne Il	e Se	er Th	ır Th	ır Va	al Pr	ю Гу	s Me	et Le	eu Val	
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Gln Va		Pne	Leu	Met	Mec	40	Ala	GIA	met	Asp	45	rue	Deu	пеп	
	35					40					40				
gct gt	· a = t =	act	+=+	as c	caa	+++	ata	acc	atc	tac	cac	ccc	ctt	caq	193
Ala Va	.g alg	Ala	Tur) ac	Ara	Phe	Val	Ala	Tle	Cvs	His	Pro	Leu	Gln	
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GIR TO			vai	Leu	пуѕ	120		Arg	Ser	мър	125	пец	пец	ASII	
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105

100

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Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170

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                                                                    240
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cacetgteag ttgtttgett attttatgga acagecettg gagggtacet eagtteaget 600
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                                                                    120
cgcatgtatg gaaagtctgc tcctgactgt gatggcctat gaccggtttg aggccatctg
                                                                    180
tcacccctg cactcccaag tcatcacgag cccacgactc tgtggcctct tagttttggt
                                                                    240
gtcttttttt cttagccttt tggactctca gctgcacaat ttgattgtgt tacaacttac
                                                                    300
ctgcttcaat gatgtggaaa tctctaattt tttcctgtga cccttctcaa cttctcagcc
                                                                    360
tggcctgttc tgacacctcc attaataaca tggtcgtata ttttattggt gccatatttg
                                                                     420
gttttctccc tctcttaggg atccttttct cttactataa aattatttct tccattctgc
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                                                                     540
ttgtttgctt attttatgga acagcccttg gagggtacct cagttcagct gtgtcccttt
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<223> Product = olfactory receptor
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Pł 1	ie Va	ıl As	p Il	.e C <u>y</u> 5	rs Ph	ie Al	a Se	er Tr	10 10	IT LI	:0 L7	/S Me	et Le 15	eu Va 5	1	
					agc Ser										9	7
					aca Thr										14	5
					gac Asp										19	3
					aac Asn 70										24	1
					gtc Val										28	9
					tgc Cys										. 33	7
					atc Ile										38	5
					ttg Leu										43	3
					tcc Ser 150										48	1
					GJÀ aaa										52	9
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	-	_	_	_	atc Ile					_	_		-		62	5
					gtc Val										64	9

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Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr 20 25 30

Gln Met Tyr Phe Phe Thr His Phe Val Gly Leu Asp Ser Phe Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val 85 90 95

Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Phe Cys 100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp 115 120 125

Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Cys Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Ile His Asn Ser His Ser Ser Ala Ile Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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gac ct Asp Le	tc act eu Thr 115	ccc Pro	atc Ile	ctc Leu	cga Arg	ctt Leu 120	tcg Ser	tgc Cys	aca Thr	gac Asp	acg Thr 125	tct Ser	gtg Val	aac Asn	385	
Arg Il	tt ttc le Phe 30	atc Ile	ctc Leu	act Thr	gtg Val 135	gca Ala	GJA aaa	atg Met	gtg Val	ata Ile 140	gcc Ala	acg Thr	ccc Pro	ttc Phe	433	
atc to Ile Cy 145	gc atc ys Ile	ctg Leu	gcc Ala	tcc Ser 150	tat Tyr	gct Ala	tgc Cys	atc Ile	ctt Leu 155	gta Val	gcc Ala	atc Ile	atg Met	aag Lys 160	481	
atc co	cc tct ro Ser	gca Ala	ggt Gly 165	ggc	agg Arg	aag Lys	aaa Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Tḥr	tgc Cys	agc Ser 175	tcc Ser	529	
cac ci His Le	tg tcc eu Ser	gtg Val 180	Val	gct Ala	ctc Leu	ttc Phe	tat Tyr 185	ggg	acc Thr	acc Thr	att Ile	ggg Gly 190	gtc Val	tac Tyr	577	
ctg to	gt ccc ys Pro 195	Ser	tcg Ser	gtc Val	cac His	acc Thr 200	gct Ala	gta Val	aag Lys	gag Glu	aaa Lys 205	gct Ala	tct Ser	gct Ala	625	
Val M	tg tac let Tyr 10														649	
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Leu V 1	/al Asr	Phe	Cys 5	: Lev	ı Ala	Thr	Asr	Thr 10	: Ile	Pro	Lys	Met	Leu 15	Val		
Ser I	Leu Glr	Thi 20	: Arg	g Ser	Lys	ala	25	e Ser	тут	Pro	Cys	30	Leu	Thr		

Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Val Leu Ile 35

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala 65 70 . 75 80

Pro Trp Val Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met 85 90 95

Ala Arg Leu Val Phe Cys Gly Ser Leu Lys Val Pro His Tyr Leu Cys 100 105 110

Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn 115 120 125

Arg Ile Phe Ile Leu Thr Val Ala Gly Met Val Ile Ala Thr Pro Phe 130 135 140

Ile Cys Ile Leu Ala Ser Tyr Ala Cys Ile Leu Val Ala Ile Met Lys 145 150 155 160

Ile Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180 185 190

Leu Cys Pro Ser Ser Val His Thr Ala Val Lys Glu Lys Ala Ser Ala 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 128

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<212> DNA

<213> Saimiri boliviensis

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WO 01/46262 PCT/IB00/02017

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					agc Ser												97
cag Gln	atg Met	tct Ser 35	ttt Phe	tca Ser	ata Ile	ttt Phe	ttt Phe 40	gcg Ala	tgt Cys	atg Met	gaa Glu	gac Asp 45	acg Thr	ctc Leu	ctg Leu		145
gct Ala	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtt Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His		193
					aac Asn 70												241
Ser	Val	Phe	Leu	Ser 85	ctt Leu	Leu	Ile	Ser	Gln 90	Val	His	Asn	Leu	Ile 95	Val		289
Leu	Gln	Phe	Ser 100	Cys	ttc Phe	Lys	Glu	11e 105	Lys	Ile	Ser	Asn	Phe 110	Phe	Cys		337
Asp	Pro	Ser 115	Gln	Leu	ctc Leu	Thr	Leu 120	Ser	Cys	Ser	Asp	Thr 125	Phe	Val	Asn		.385
Asn	Ile 130	Val	Thr	Asn	ttc Phe	Phe 135	Ala	Ala	Val	Phe	Gly 140	Phe	Leu	Pro	Ile		433
Ser 145	Gly	Ile	Phe	Phe	tct Ser 150	Tyr	Tyr	Lys	Ile	Ala 155	Pro	Ser	Ile	Leu	Arg 160		481
Val	Pro	Leu	Ser	Ser 165		Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Cys	Ser 175	Ser		529
His	Leu	Ala	Val 180	Val	Cys	Leu	Phe	185	Gly	Thr	Val	Ile	Gly 190	Val	tac Tyr		577
			Ser					Arg					Ala		gtg Val		625
		Thr			act Thr												646

WO 01/46262 PCT/IB00/02017

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Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Pro Ser Ile Leu Arg 145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175 His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 

Met Tyr Thr Val Val Thr Pro 

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aat at Asn Il														97
cag at Gln Il														145
act gt Thr Va 50	l Met													193
tac ac Tyr Th 65														241
tcc tg Ser Tr		Leu												289
ctg cg Leu Ar														337

WO 01/46262									13	7					PCT	/IB00/02017
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			ata Ile						38	85
			ttg Leu						4:	33
			tct Ser 150						4.	81
			Gly						52	29
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			act Thr						6	25
~ -	_		 gtc Val						6	49

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5

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60

138

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 70 75

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys 105 100

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 135

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 155 150

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr . 180 185

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Ala Leu

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 132

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		-			agc Ser						-	_					97
_					cta Leu			-		_	_			-	_		145
					gac Asp									_			193
		_			aac Asn 70		_	_	_		_	-		_	_		
			_	-	gcc Ala	_											289
_					tgc Cys		-	_	-						_		337
_			_	_	ata Ile			-	_		_						385
					ttg Leu												433
					ser 150			_		-				-	. —		481
Ile	Ser	Ser	Ala	Gln 165	GJÅ aàa	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Cys	Ala 175	Ser		529
His	Ile	Leu	Ile 180	Val	tcc Ser	Leu	Phe	Tyr 185	Gly	Thr	Leu	Leu	Gly 190	Val	Tyr		577
Leu	Ser	Ser 195	Ala	Ala	Thr	Gly	Asn 200								ttg Leu	•	625
	_				gtc Val												649

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Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

170

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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Ph	c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val															
1				5					10	)				15	5	
aat	atc	cag	aca	cac	agc	aaa	gtc	atc	acc	ttt	gca	ggc	tgc	atc	acc	97
Asn	Ile	Gln	Thr	His	Ser	Lys	Val	Ile	Thr	Phe	Ala	Gly	Cys	Ile	Thr	
			20					25					30			
cag	ata	ggc	cat	tgc	cta	ctc	ttt	gca	gca	ttg	gac	atc	ttt	atg	ctg	145
			His													
		35					40					45				
act	gtg	atg	gcc	tat	gac	cgg	tat	gtg	gcc	atc	tgt	cac	CCC	ctg	cac	193
			Ala													
	50			_	_	55	_				60					
tac	aca	atc	acc	att	aac	ccc	aga	ctg	tgt	gga	ctg	ctg	gtt	ctg	gca	241
			Thr													
65					70				-	75					80	
tcc	taa	atc	ctg	agt.	acc	cta	aat	tcc	tca	tta	caa	acc	tta	ata	ata	289
			Leu													
UCI	115	110		85				502	90					95		
				0.5					,							
cta	כממ	ctt	tcc	ttc	tac	aca	gac	tta	gaa	atc	CCC	cac	ttt	tto	tac	337
_			Ser		-		-									
neu	πιy	TIEU	100	1110	Cys	1114	nap	105			-10	*****	110		-3-5	
			100					103					110			

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 481 aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 150 155 atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct 529 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170 165 cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac 577 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185 180 ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg 625 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 195 649 gtg atg cac aca gtg gtc acc ccc

Val Met His Thr Val Val Thr Pro 215 210

<210> 135 <211> 216 <212> PRT <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val

10

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 25

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 45 35 40

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60

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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 75 70

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu 135

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 155 150

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr 185 180

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 200 205 195

Val Met His Thr Val Val Thr Pro 215 210

<210> 136

<211> 646

<212> DNA

<213> Saimiri sciureus

<220>

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<222> (2)..(646)

<223> Product = olfactory receptor

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Low Ala Asp Tie Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Tie Val

Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val 1 5 10 15																	
aac Asn	att Ile	caa Gln	act Thr 20	cac His	agc Ser	aga Arg	gtc Val	atc Ile 25	gcc Ala	tat Tyr	gcg Ala	agc Ser	tgc Cys 30	ctg Leu	aca Thr	9	7
					atc Ile											14	5
gct Ala	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgg Arg 55	ttt Phe	gtt Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctg Leu	cac His	<b>19</b>	3
					aac Asn 70											24	. <b>1</b>
					ctt Leu											28	9
Leu	Gln	Phe	Ser 100	Суѕ	ttc Phe	Lys	Glu	Ile 105	Lys	Ile	Ser	Asn	Phe 110	Phe	Cys	33	7
Asp	Pro	Ser 115	Gln	Leu	ctc Leu	Thr	Leu 120	Ser	Cys	Ser	Asp	Thr 125	Phe	Val	Asn	38	₹5
					ttc Phe											43	13
Ser 145	Gly	Ile	Phe	Phe	tct Ser 150	Tyr	Tyr	Lys	Ile	Ala 155	Ser	Ser	Ile	Leu	Arg 160		31
Val	Pro	Leu	Ser	Ser 165	GJÀ aaa	Lys	Tyr	Lys	Ala 170	Phe	Ser	Thr	Cys	Ser 175	Ser		29
His	Leu	Ala	Val 180	Val	tgc Cys	Leu	Phe	Tyr 185	Gly	Thr	Val	Ile	Gly 190	Val	Tyr		77
Leu	Gly	Ser 195	Ser	Met	gca Ala	Ser	200	Arg					Ala				25
		Thr			act Thr											64	46

<210> 137 <211> 215 <212> PRT <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(646) <223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902 <400> 137 Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val 10 Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 40 35 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55 50 Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 80 70 75 65 Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg

155

150

145

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190

Met Tyr Thr Val Val Thr Pro 210 215

<210	> 13	38														
<211:	> 6	49														
<212	> DI	NΑ		•												
<213	> S	Saimiri sciureus														
<220	>															
<221	> m	isc_	feat	ıre												
<222	> (	(1)(649)														
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<220	>															
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<400	> 1	38														
c tt	c tc	t ga	c ct	c tg	c tt	c tc	t tc	t gt	g ac	c at	t cc	a aa	g tt	g tt	a cag	49
Ph	e Se	r As	p Le	u Cy	s Ph	e Se	r Se	r Va	l Th	r Il	e Pr	о Ly	s Le	u Le	u Gin	
1			_	5					10					15		
aac	atq	cag	agc	caa	gac	cca	tcc	atc	CCC	tat	gcg	ggc	tgc	ctg	acc	97
Asn	Met	Gln	Ser	Gln	Asp	Pro	Ser	Ile	Pro	Tyr	Ala	Gly	Cys	Leu	Thr	
			20					25					30			
													•			
caq	ato	tac	ttc	ttc	ttg	tat	ttt	tcg	gat	cta	gag	agc	ttc	ctc	ctt	145
Gln	Met	Tvr	Phe	Phe	Leu	Tyr	Phe	Ser	Asp	Leu	Glu	Ser	Phe	Leu	Leu	
		35					40					45				
	•															
ata	acc	atq	acc	tat	gac	cgc	tac	gtg	gcc	atc	tgc	ctc	CCC	cta	cat	193
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Leu	Pro	Leu	His	
	50	_		_	_	55					60					
tac	acc	acc	atc	atq	agc	ccc	atg	ctg	tct	cgc	tcc	ctg	gtg	gcg	ctg	241
Tyr	Ala	Thr	Ile	Met	Ser	Pro	Met	Leu	Ser	Arg	Ser	Leu	Val	Ala	Leu	
65	****				70					75					80	
05									,							
tee	taa	ata	cta	acc	acc	ttc	cat	gcc	atg	ttg	cac	act	tta	ctc	atg	289
Cor	Trans	Wal	Len	Thr	Thr	Phe	His	Ala	Met	Leu	His	Thr	Leu	Leu	Met	
Der	110	VUI		85					90					95		
				0.5												
~~~	2~~		cat	+++	tgt	gca	gac	aat	ata	atc	ctc	cac	ttt	ttc	tgt	337
31-	299	LLY	Δ~~	Dhe	Cys	Ala	Asp	Asn	Val	Ile	Leu	His	Phe	Phe	Cys	
итg	Arg	neu		r me	2,3			105					110			
			100					100								

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	gcc tgc tct gac act Ala Cys Ser Asp Thr 125	
	ggc ctc att ctt gtc Gly Leu Ile Leu Val 140	
	cga att gtc ttc tcc Arg Ile Val Phe Ser 155	
Val Pro Ser Ser I	aag gcc gtc tct act Lys Ala Val Ser Thr 170	
	tat ggg act gtt att Tyr Gly Thr Val Ile 185	

Val Met Tyr Thr Val Met Ala Pro
210 215

<210> 139
<211> 216
<212> PRT
<213> Saimiri sciureus
<220>
<221> misc_feature

205

tta tgc cca tca gct aat aat tct act cta aag gag act gtc atg gct Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala

200

195

<222> (1)..(649)

gtg atg tac act gtg atg gcc ccc

625

649

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His 50 55 60

Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu 70 65

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 90

Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys 105 100

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn 120

Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu 135

Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys 155 150

Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser 170 175 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr . 180 185

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala 205 195 200

Val Met Tyr Thr Val Met Ala Pro 210

<210> 140

<211> 646

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 9521; gene = SSC34; Accession DDBJ/EMBL/GenBank = AF127904

<220>

<221> CDS

<222> (2)..(646) <223> Product =olfactory receptor

<400> 140

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Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val 1 5 10 15	
aac att caa act cac agc aga gtc atc gcc tat gcg agc tgc ctg aca Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 20 25 30	97
cag atg tct ttt tca atc ttt ttt gcg tgt atg gaa gac acg ctc ctg Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 35 40 45	145
gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60	193
tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 65 70 75 80	241
tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 90 95	289
tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 110	337
gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 120 125	385
aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 130 135 140	433
tca ggg atc ttt ttc tct tac tat aaa att gcc tcc tcc att ctg aga Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg 145 150 155 160	481
gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175	529
cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc att gga gtg tac His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190	577
ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val 195 200 205	625
atg tac aca gtg gtc act ccc Met Tyr Thr Val Val Thr Pro 210 215	646

<210> 141 <211> 215 <212> PRT <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(646) <223> Taxon = 9521; gene = SSC34; Accession DDBJ/EMBL/GenBank = AF127904 Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr 25 Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu 40 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val 75 · 65 Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val 85 Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys 100 105 Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn 115 Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile 135 130 Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg

155

150

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser

145

WO 01/46262 PCT/IB00/02017

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val . 195 200 205

Met Tyr Thr Val Val Thr Pro 210 215

<210> 142 <211> 649 <212> DNA <213> Saimiri boliviensis <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 27679; gene = SB064; pseudogene; Accession DDBJ/EMBL/GenBank = AF127905 <400> 142 ctttgtcgat ttctgttatt ccaccaccgt tatacccaaa ctgctggaga acitggttgt 60 ggaagacaga agcatctcct tcacaggatg cgtcatgcaa ttcttttttg ccagcatatt 120 tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tggtggtgtg 180 ttaccctctg ctctacacag ttgcaatgtc ccagaggett ttctttttgt tagtggctac 240 atcatacttc agggtgacag tctgtttctt gacaattacc ttctttctcc tggaattatc 300 360 cttcagagga aataatatca ttaataactt tgtgtgtgag cctgctgcca ttgttgctgt gccatgcttt gacccctaca tgagccagga aatcattttc atttctgcca cattcaatga 420 aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat 480 gatgccttcc actggggggc gcataaaagc atgcgcgacc tgttcctccc agctgaccgc 540 cattatcatt ttccatggga ccatctcttt tctctattgt gttcctaact ccaaaagttc 600 649 atggctcatg gtcaaggtgg gctctatctt ttacacagtg gtcatcccc

<210> 143

<211> 649

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906

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										ır Il					eu Ser	47
			aca Thr 20													97
			ttt Phe													.145
			gcc Ala													193
			atc Ile													241
Ser	Trp	Ile	atg Met	Ser 85	Ala	Leu	His	Ser	Leu 90	Thr	Glu	Ser	Leu	Met 95	Ala	289
Leu	Ser	Leu	ctc Leu 100	Phe	Суѕ	Thr	Asp	Leu 105	Lys	Ile	Leu	His	Phe 110	Phe	Суз	337
Glu	Leu	Asn 115	cag Gln	Ile	Ile	His	Ile 120	Ala	Суѕ	Ser	Asp	Thr 125	Cys	Leu	Asn	385
Asn	Leu 130	Val	atg Met	Tyr	Leu	Ser 135	Ala	Val	Leu	Leu	Gly 140	Gly	Gly	Pro	Leu	433
Ala 145	Gly	Ile	ctg Leu	Tyr	Ser 150	Tyr	Ser	Lys	Ile	Ala 155	Ser	Ser	Ile	Arg	Ala 160	481
			'gct Ala													529
			gtt Val 180	_					-							577
ctg	agt	tct	gct	gca	acc	cac	aac	tca	ctc	tca	agt	aca	gca	gcc	tcg	625

649

Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser

195 200 205

gtg atg tac act gtg gtc acc ccc Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 144

<211> 216

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906

Phe Val Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Thr Leu Ser

Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr 25

Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu 35 40

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg 50 55

Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val 75

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala 85

Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Phe Cys 100 105

Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn 115 120

Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala

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	154	

155 160 145 150 Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 170 165 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr 185 Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser 200 195 Val Met Tyr Thr Val Val Thr Pro 210 215 <210> 145 <211> 649 <212> DNA <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor <400> 145 c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val 1 aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr 20 25 145 cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 35 40 193 act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 70 75 65

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val 289

									15.	5							
				85					90					95			
ctg Leu	cgg Arg	ctt Leu	tcc Ser 100	ttc Phe	tgc Cys	aca Thr	gac Asp	ttg Leu 105	gaa Glu	atc Ile	ccc Pro	cac His	ttt Phe 110	ttc Phe	tgc Cys		337
												act Thr 125					385
gat Asp	gtg Val 130	gtg Val	atg Met	tat Tyr	ttg Leu	gca Ala 135	gct Ala	atg Met	ctg Leu	ctg Leu	ggc Gly 140	ggt Gly	ggt Gly	ccc Pro	ctc Leu		433
aca Thr 145	gga Gly	att Ile	att Ile	tac Tyr	tct Ser 150	tac Tyr	tct Ser	aag Lys	ata Ile	gtt Val 155	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala 160		481
atc Ile	tca Ser	tca Ser	gct Ala	cag Gln 165	Gly	aag Lys	tac Tyr	aag Lys	gcg Ala 170	ttt Phe	tcc Ser	acc Thr	tgt Cys	gca Ala 175	tct Ser		529
				Val								cta Leu					577
												gct Ala 205					625
					gtc Val												649
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<40 Phe		146 Asp	Ile	Cys 5	Phe	Val	Ser	Thr	Thr 10	Val	Pro	Lys	Met	Leu 15	Val		
Asn	Ile	Gln	Thr 20	His	Ser	. L ys	Val	11e 25	Thr	Phe	Ala	Gly	Cys	Ile	Thr		

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His . 50 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala 65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn 115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu 130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

<210> 147

<211> 487

<212> DNA

<213> Papio hamadryas

<220>

<221> misc_feature

<222> (1)..(487)

137													
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221> CDS													
<222> (2)(487)													
<223> Product = olfactory receptor													
<400> 147													
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Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met													
1 5 10 15													
ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat	97												
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His													
20 25 30													
gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac	145												
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp													
35 40 45													
aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg	193												
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu													
50 55 60													
300 030 000 000 000 000	241												
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly													
65 70 75 80													
	289												
ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala	203												
85 90 95													
03													
cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc	337												
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys													
100 105 110													
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	385												
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe													
115 120 125													
tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct	433												
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser	433												
130 135 140													
act cta aag gag act gtt atg gct atg atg tac act gtg gtg acc ccc	481												
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro													
145 150 155 · 160													
atg ctg	487												
Met Leu													

<210> 148 <211> 162 <212> PRT

PCT/IB00/02017 WO 01/46262 158

<213> Papio hamadryas

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<400> 148

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 1 . 5 10

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40 -

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 70 75

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 90

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 105

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 130 135

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 150 155

Met Leu

<210> 149

<211> 486

<212> DNA

<213> Papio hamadryas

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<210> 150

<211> 161

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<213> Papio hamadryas

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<400> 150

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Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30

Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg 35 40 45

Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80

Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile 85 90 95

Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg 100 105 110

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140

Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro 145 150 150 155 160

Met

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<210> 152 <211> 482

<212> DNA

<213> Papio hamadryas

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179719

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1	
tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat	97
Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His	
20 25 30	
ggg tot atc cag gcc acc ctg acc ttc cgc cta ccc tat tgt ggg ccc	145
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro	
35 40 45	
	102
aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg	193
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 50 60	
50 55 60	
gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc	241
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile	
65 70 75 80	
•	
gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat gcc	289
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala	
85 90 95	
aac ata gtc cat gcc atc ctg aag ata cgc acc act gat ggg agg cgc	337
Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg	
100 105 110	
	305
cgg gcc ttc tct acc tgt ggc tcc cac cta act gtg gtc aca gtc tac Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr	385
115 120 125	
tat gtt ccc tgt att ttc atc tac ctt agg gct ggc tcc aag agc ccc	433
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro	
130 135 140	
ctg gat ggg gca gtg gct gtg ttt tac act gtt gtc act cca ttc ctg	481
Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu	
145 150 155 160	

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<210> 154 <211> 160 <212> PRT <213> Papio hamadryas <220> <221> misc_feature <222> (1)..(481) <223> Taxon = 9557; gene = PPA137; Accession DDBJ/EMBL/GenBank = AF179720 <400> 154 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg 10 5 Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His 20 25 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro 40 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu 55 50 Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile 70 65 Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 85 Asn Ile Val His Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg Arg 105 Arg Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Thr Val Tyr 120 115 Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Ser Pro 130 135 Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu 155 150 145 <210> 155 <211> 487

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	al Al	la II	le Cy		s Pi	ro Le	eu Le	eu Ty			al I	le Me	et Ti	ar As	sn Gly	
1				5					10)				15	5	
ctg	tgc	atc	cgg	cta	tta	gtc	ttg	tca	ttt	gta	ggt	ggc	ttc	ctt	cat	97
Leu	Cys	Ile	Arg	Leu	Leu	Val	Leu	Ser	Phe	Val	Gly	${\tt Gly}$	Phe	Leu	His	
			20					25					30			
gcc	tta	att	cat	gaa	ggc	att	tta	ttc	aga	tta	acc	ttc	tgt	aat	tct	145
Ala	Leu		His	Glu	Gly	Ile	Leu	Phe	Arg	Leu	Thr	Phe	Cys	Asn	Ser	
		35					40					45				
aac	ata	ata	cat	cac	ttt	tac	tgt	gac	att	atc	cca	ttg	tta	acg	att	193
Asn		Ile	His	His	Phe		Cys	Asp	Ile	Ile		Leu	Leu	Thr	Ile	
	50					55					60					
tcc	tgt	act	gac	cct	tct	att	aat	ttt	tta	atg	ctt	ttt	att	ttg	tct	241
	Cys	Thr	Asp	Pro	_	Ile	Asn	Phe	Leu		Leu	Phe	Ile	Leu	Ser	
65					70					75					80	
				gta												289
Gly	Ser	Ile	Gln	Val	Phe	Thr	Ile	Leu		Val	Leu	Val	Ser	_	Ala	
				85					90					95		
				aca												337
Phe	Val	Leu		Thr	Ile	Leu	Lys		Lys	Ser	Val	Lys		Ile	Arg	
			100					105					110			
aaa	gcc	ttt	tcc	acc	tgt	gga	gcc	cat	ctc	ttc	tct	gtc	tgt	tta	tac	385
Lys	Ala		Ser	Thr	Cys	Gly		His	Leu	Phe	Ser	Val	Cys	Leu	Tyr	
		115					120					125				_
				ctc												433
Tyr		Pro	Leu	Leu	Phe		Tyr	Val	Gly	Pro		Ser	Pro	Gln	Ala	
	130					135					140					
				atg												481
	Asp	Gln	Asp	Met		Glu	Cys	Val	Phe		Thr	Val	Ile	Ile		
145					150					155					160	
ttc	tta															487
Phe	Leu															

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Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser 35 . 40 45

Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile 50 55 60

Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser 65 70 75 80

Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala 85 90 95

Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg

Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr 115 120 125

Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala 135 140

Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro 145 150 155 160

Phe Leu

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_			_	-			-			-					ag cgg	49
Va 1	.I A.	La I.	re cz	7s As 5	an Pi	co Le	eu Le	eu Ty	/r Me		at Va	al Va	al Se	er Ai 15	rg Arg	
ctc	tac	ctc	ctg	cta	ata	tcc	ctc	aca	tac	ctc	tat	aac	+++	tct	aca	97
Leu																٥,
	_		20					25	-		-	_	30			
gct	att	gtg	gtt	tca	cct	tgt	ata	ttc	tct	atg	tct	tat	tgc	tct	tct	145
Ala	Ile		Val	Ser	Pro	Cys		Phe	Ser	Met	Ser	_	Cys	Ser	Ser	
		35					40					45				
aat	ata	atc	aat	cat	ttt	tac	tgt	gat	att	gca	cct	ctg	tta	gca	tta	193
Asn		Ile	Asn	His	Phe	_	Cys	Asp	Ile	Ala		Leu	Leu	Ala	Leu	
	50					55					60					
tct	tgc	tct	gat	act	tac	tta	сса	gaa	gca	ata	gtc	ttc	ata	tct	gca	241
Ser	Cys	Ser	Asp	Thr	Tyr	Leu	Pro	Glu	Ala		Val	Phe	Ile	Ser		
65					70					75					80	
gca	aca	aat	ttg	gtt	ttt	tcc	atg	att	aca	gtt	cta	gta	tct	tat	ttc	289
Ala	Thr	Asn	Leu		Phe	Ser	Met	Ile		Val	Leu	Val	Ser	_	Phe	
				85					90		-			95		
aat	att	gtt	ttg	tcc	att	cta	agg	atg	cat	tca	tca	gaa	gga	agg	aaa	337
Asn	Ile	Val	Leu	Ser	Ile	Leu	Arg		His	Ser	Ser	Glu	_	Arg	Lys	
			100					105					110			
aaa	gcc	ttt	tcc	acc	tgt	gct	tca	cat	atg	atg	gca	gtc	aca	gtt	ttc	385
Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Met	Met	Ala	Val	Thr	Val	Phe	
		115					120					125				
tat	ggg	aca	atg	ctg	ttc	atg	tat	ttg	cag	ccc	caa	acc	aac	cac	tca	433
Tyr	Gly	Thr	Met	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Gln	Thr	Asn	His	Ser	
	130					135					140					
ctg	gat	act	gat	aag	atg	gct	tct	gtg	ttt	tac	aca	ttg	gtg	att	cct	481
	Asp	Thr	Asp	Lys		Ala	Ser	Val	Phe		Thr	Leu	Val	Ile		
145					150					155					160	
atg	ctg															487

Met Leu

<210> 158

<211> 162

<212> PRT

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<222> (1)..(487)

<223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722

<400> 158

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20

Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr 25

Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser

Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu

Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala 70

Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe 90

Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys 100 105

Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe 120 125 115

Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser 130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro 150 145

Met Leu

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<210	> 1	.59								•						
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<222			(487													. = 1 5 0 5 0 0
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<221		DS.										•				
<222			(487	•											•	
<223			ıct =	o T I	acto	ry r	ecer	otor								
<400	_	.59											~ ~			49
t gt	g go	:C at	C TO	ים בנ וכ בנ	.c .cc	C CU	.g ca	ic ta	c ac	c gc ייי	:C at	o Mo	y as	ye et	c atg	4.5
	LAL	.a 1.	le Cy		ie Pi	о те	u ni	.s Ty			.a li	Le Me	:	15	o Met	
1				5					10	,				т.	,	
ata	+~+	ata	gcc	a+a	ata	aca	cta	tee	taa	ata	cta	acc	acc	ttc	cat	97
Lou	Cyc	Lou	Ala	Len	Wal	Δla	T.em	Ser	Trun Trun	Val	Len	Thr	Thr	Phe	His	
пеа	Cys	пец	20	Deu	V (4.4.	1114	200	25		,			30			
			20													
acc	ato	tta	cac	act	tta	ctc	ato	acc	agg	tta	tat	ttt	tac	qca	gac	145
			His													
		35					40		•		•	45	-		_	
		-														
aat	ata	atc	ccc	cac	ttt	ttc	tgt	gat	atg	tct	gct	ctg	ctg	aag	ctg	193
			Pro													
	50					55	-	_			60		•			
gcc	tgc	tct	gac	act	cga	gtc	aat	gaa	ttg	gtg	ata	ttt	atc	atg	gga	241
			Asp													
65					70 .				•	75					80	
			ctt													289
Gly	Leu	Ile	Leu	Val	Ile	Pro	Phe	Leu		Ile	Leu	Gly	Ser		Ala	
				85					90					95		
										_						227
			tcc													337
Arg	Ile	Val	Ser	Ser	Ile	Leu	ГЛЗ		Pro	Ser	Ser	Lys		тте	Cys	
			100					105					110			
										L L			-			305
			tct													385
Lys	Ala		Ser	Thr	Cys	GIY		HIS	ren	Ser	vaı		Ser	ьeu	Pile	
		115					120					125				
			- 4-4-									~~+	224	-a-	tat	433
tat	ggg	acc	att	acc	ggt	CEC	tac	בבכ	tgc	CCa D	Con	310	300	agı	502	423
ıyr		ınr	Ile	TTG	стХ			FIIE	cys	LTO	140		ווכת	Set	Det	
	130					135					T#O					
224	~	227	gag	201	~++	a+~	~~+	2+~	2+~	tec	act	αtα	ata	acc	ccc	481
			gag Glu													401
IUL	ьeи	пĀг	GIU	THE	val	mec	GTA	met	met	TÄŢ	TIIT	val	val	1111	ETO	

WO 01/46262		169	PCT/IB00/02017
145	150	155	160
atg ctg Met Leu			487
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Leu Cys Leu Ala Leu 20	Val Ala Leu	Ser Trp Val Leu Thr 25	Thr Phe His
Ala Met Leu His Thr	Leu Leu Met	Ala Arg Leu Cys Phe	Cys Ala Asp
35	40	45	
Asn Val Ile Pro His	Phe Phe Cys	Asp Met Ser Ala Leu	Leu Lys Leu
50	55	60	
Ala Cys Ser Asp Thr	Arg Val Asn	Glu Leu Val Ile Phe	Ile Met Gly
65	70	75	80
Gly Leu Ile Leu Val	Ile Pro Phe	Leu Leu Ile Leu Gly	Ser Tyr Ala
85		90	95
Arg Ile Val Ser Ser	Ile Leu Lys	Val Pro Ser Ser Lys	Gly Ile Cys
100		105	110
Lys Ala Phe Ser Thr	Cys Gly Ser	His Leu Ser Val Val	Ser Leu Phe
115	120	125	
Tyr Gly Thr Ile Ile	Gly Leu Tyr	Phe Cys Pro Ser Ala	Asn Ser Ser
130	135	140	

Met Leu

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<400>		61					•						•			
			c ta	t aa	ים ככ	c tt	αaa	c ta	it ac	a ac	c at	c at	a ac	rt ca	a cct	49
t 909	ים אם דגו	~ T1	.c cy	e ta	e Dr	o te	nı Ac	n Tu	rr A1	a mh	r Tl	e Me	et Se	er Gl	n Pro	
	LAI	.a 11	.е су	_	5 11	.0 10		3	10					15		
1				5					10	,				10	•	
								~~+	~~~	n++	ata	~~=	+++	ata	cat	97
atg i	tgt	gga	TTC	ctg	atg	999	gug	31-	999	710	Lou	77.	Dho	7721	ui e	٥.
Met (Cys	GIA		теп	met	GTĀ	var		GIY	TTE	пеп	GIY		val	HTS	
			20					25					30			
																145
gga g	ggg	atc	cag	act	ctg	ttc	ata	gcc	cag	tta	cca	TTC	tgt	ggc	CCC	145
Gly	Gly	Ile	Gln	Thr	Leu	Phe		Ala	Gln	Leu	Pro		Cys	GTĀ	Pro	
		35					40					45				
aat g	gtc	atc	gac	cac	ttt	atg	tgt	gat	tta	gta	cct	ctt	cta	gag	ctg	193.
Asn '	Val	Ile	Asp	His	Phe	Met	Cys	qaA	Leu	Val	Pro	Leu	Leu	Glu	Leu	
!	50					55					60					
gcc	tgc	aca	gac	act	cac	acc	ttg	ggg	cct	ctg	ata	gct	gcc	aac	agt	241
Ala	Cys	Thr	Asp	Thr	His	Thr	Leu	Gly	Pro	Leu	Ile	Ala	Ala	Asn	Ser	
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gga	tca	tta	tat	ttc	ctc	att	ttt	tcc	atq	ctg	gtt	gct	tcc	tat	gtc	289
Gly	Ser	Len	Cvs	Phe	Leu	Ile	Phe	Ser	Met	Leu	Val	Ala	Ser	Tyr	Val	
013			-1-	85					90					95		
				-					• •							
atc	a t a	cta	taa	tac	cta	add	act	cat	atc	tct	gaa	aaa	cat	cac	aaa	337
Ile																
TIG	TTE	neu		261	Deu	, mg	****	105		001		2	110			
			100					103								
				.		L L			444			-+a	++=	++~	+++	385
gct																303
Ala	Leu			Cys	Thr	ser		тте	Pne	vaı	vaı			PHE	FIIE	
		115					120					125				
																422
gtc	cct	tgt	tca	tac	ctg	tat	cta	aga	cct	cta	acc	tcc	ttc	CCC	act	433
Val	Pro	Суз	Ser	Tyr	Leu	Tyr	Leu	Arg	Pro	Leu		Ser	Phe	Pro	Thr	
	130					135					140					

WO 01/46262 PCT/IB00/02017

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Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145 150 155

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Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro 35 40 45

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu 50 55 60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser 65 70 75 80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 85 90 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
100 105 110

Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr 130 135 140

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atg ctg 487 Met Leu

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<400> 164

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Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile 20 25 . 30

Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser 35 40 45

Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 50 55 60

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala 65 70 75 80

Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile 85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro 145 150 155 160 Met Leu

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_	-			-	-		-								o Trp	43
1				5					10					15	_	
							٠,									•
				atg												97
Ala	Суѕ	Met		Met	Val	Gly	Thr		Trp	Leu	Thr	Gly		Ile	Thr	
			20					25					30			
acc	acc	acc	cat	gcc	ttc	ctc	atc	ttc	tct	cta	cct	ttt	ccc	age	cac	145
_				Ala										-	_	
		35					40					45				
				cac			_	_		_		_	_		_	193
Pro		IIe	Pro	His	Phe	Leu 55	Cys	Asp	IIe	Leu	Pro 60	Val	Leu	Arg	Leu	
	50					33					80					•
gca	agt	gct	ggg	aag	cac	agg	agc	gag	atc	tct	gtg	atg	aca	gcc	act	241
Ala	Ser	Ala	Gly	Lys	His	Arg	Ser	Glu	Ile	Ser	Val	Met	Thr	Ala	Thr	
65					70					75					80	
			_ 1-1-		- 4		4.4		_ 1							200
-	_			atg Met					_		_					289
val	vaı	rne	TTE	85	тте	PIO	FIIE	Ser	90	TT6	vaı	1111	Ser	95	116	
				•••					-							
cgc	atc	ctg	gga	gcc	atc	cta	gcg	atg	gcc	tcc	acc	cag	agc	cgc	cgc	337
Arg	Ile	Leu	Gly	Ala	Ile	Leu	Ala	Met	Ala	Ser	Thr	Gln	Ser	Arg	Arg	
			100					105					110			
~~~		++-	+	200	+~~	taa	+	ant	a+~	a+ a	~+~	~+~	+	ata.	.htg	385
				acc Thr												303
_,	,	115	<b>D</b> 02		0,70	-	120		200	200	102	125				
ttt	gga	aca	gcc	agc	atc	acc	tac	atc	cgg	ccg	cag	gca	ggc	tcc	tct	433
Phe		Thr	Ala	Ser	Ile		Tyr	Ile	Arg	Pro		Ala	Gly	Ser	Ser	
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				Arg												301,
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145 150 155 160

487 atg ctc Met Leu

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Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 55

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 70 75

Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile 90

Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg

Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe 115 120

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135

Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro 150 155 145

Met Leu

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1				5					10	)				1	5	
				gtg												97
Leu	Cys	Leu		Val	Val	Thr	Leu		Trp	Val	Leu	Thr		Phe	His	
	•		20					25					30			
				act												145
Ala	Met		His	Thr	Leu	Leu		Ala	Arg	Leu	Cys		Cys	Ala	Asp .	
		35					40					45				
				cac												193
Asn		тте	Pro	His	Phe		Cys	Asp	Met	Ser		Leu	Leu	Lys	Leu	
	50					55					60					
				act												241
	Cys	ser	Asp	Thr		Val	ASI	GIU	пр		тте	Pne	тте	Met		
65					70					75					80	
				gtc												289
GIY	ьеп	TTE	val	Val	тте	Pro	Pne	ren		тте	Leu	GIY	Ser	_	Ala	
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				<b>.</b>												
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Arg	тте	vaı		Ser	тте	Leu	ьуѕ		Pro	ser	Ser	rās	_	IIe	Cys	
			100					105					110			
			A A.									,				
				act					_					_		385
гЛS	Ala		Ser	Thr	Cys	GLY		His	Leu	Ser	Val		Ser	Leu	Phe	
		115					120					125				
<b>.</b>																
				att												433
Tyr	_	Thr	Val	Ile	Gly		Tyr	Leu	Cys	Pro		Ala	Asn	Ser	Ser	
	130					135					140					

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Met Leu

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gcc at Ala Me											_				145
aat gt Asn Va 50	l Ile														193
gcc tg Ala Cy 65															241
ggg ct															289
aga at Arg Il															337
aag go Lys Al		Ser												_	385

WO 01/46262	170	-	PCT/IB00/02017

tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct 433 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 135 140 130 act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 155 145 150 487 atg ctg Met Leu <210> 170 <211> 162 <212> PRT <213> Pan troglodytes <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728 <400> 170 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 10 Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40 Asn Val Ile Pro His Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly 70 Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 90 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 115 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser 130

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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 ccatctgctt tctgtctcat tgtactacgg aactctgatc ttcatgtatg tgcgtcctgc
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<223> Product = olfactory receptor
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gtc tgt gcc cta atg Val Cys Ala Leu Met 20	ctt gca ttg tgc Leu Ala Leu Cys 25	tgg gtc ctc acc aa Trp Val Leu Thr As 30	n Ile Ile						
gcc ctg act cac acg Ala Leu Thr His Thr 35	ttc ctc atg gct Phe Leu Met Ala 40	cgg ttg tcc ttc tg Arg Leu Ser Phe Cy 45	rt gtg act 145 rs Val Thr						
ggg gaa att gct cac Gly Glu Ile Ala His 50	ttt ttc tgt gac Phe Phe Cys Asp 55	atc act cct gtc ct Tle Thr Pro Val Le 60	g aag ctg 193 u Lys Leu						
tca tgt tct gac acc Ser Cys Ser Asp Thr 65	cac atc aac gag His Ile Asn Glu 70	atg atg gtt ttt gt Met Met Val Phe Va .75	c ttg gga 241 al Leu Gly 80						
ggc acc gta ctc atc Gly Thr Val Leu Ile 85	gtc ccc ttt tta Val Pro Phe Leu	tgc att gtc acc to Cys Ile Val Thr Se 90	cc tac atc 289 er Tyr Ile 95						
cac att gtg cca gct His Ile Val Pro Ala 100	atc ctg agg gtc Ile Leu Arg Val 105	Arg Thr Arg Gly Gl	gg gtg ggc 337 Ly Val Gly 10						
aag gcc ttt tcc acc Lys Ala Phe Ser Thr 115	tgc agt tcc cac Cys Ser Ser His 120	c ctc tgc gtt gtt tg Leu Cys Val Val Cy 125	gt gtg ttc 385 ys Val Phe						
tat ggg acg ctc ttc Tyr Gly Thr Leu Phe 130	agt gcc tac ctg Ser Ala Tyr Let 135	g tgt cct ccc tcc at 1 Cys Pro Pro Ser I 140	tt gcc tct 433 le Ala Ser						
gaa gag aag gac att Glu Glu Lys Asp Ile 145	gca gca gct gca Ala Ala Ala Ala 150	a atg tac acc ata go a Met Tyr Thr Ile Vo 155	al Thr Pro 160						
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Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly 75 70

Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile 95 85 90

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly 105

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe

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ctc Leu	tgt Cys	gcc Ala	tct Ser 20	ctg Leu	gta Val	gct Ala	gca Ala	cct Pro 25	tgg Trp	gtc Val	att Ile	gcc Ala	att Ile 30	ttg Leu	aac Asn	97
cct Pro	ctc Leu	ttg Leu 35	cac His	act Thr	ctt Leu	atg Met	atg Met 40	gcc Ala	cat His	ctg Leu	cac His	ttc Phe 45	tgc Cys	tct Ser	gat Asp	145
					ttc Phe											193
tcc Ser 65	tgt Cys	tcc Ser	aac Asn	acc Thr	agt Ser 70	ctt Leu	aat Asn	cag Gln	ttg Leu	agt Ser 75	gtt Val	ctg Leu	gct Ala	acg Thr	gtg Val 80	241
Gly ggg	ctg Leu	atc Ile	ttt Phe	gtg Val 85	gta Val	cct Pro	tca Ser	gtg Val	tgt Cys 90	atc Ile	ctg Leu	gta Val	tcc Ser	tat Tyr 95	atc Ile	289
ctc Leu	att Ile	gtt Val	tct Ser 100	gct Ala	gtg Val	atg Met	aaa Lys	gtc Val 105	cct Pro	tct Ser	gcc Ala	caa Gln	gga Gly 110	aaa Lys	ctc Leu	337
aag Lys	gct Ala	ttc Phe 115	tct Ser	atc Ile	tgt Cys	gga Gly	tct Ser 120	cac His	ctt Leu	gcc Ala	ttg Leu	gtc Val 125	att Ile	ctt Leu	ttc Phe	385
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<223> Taxon = 9598; gene = PTR206; Accession DDBJ/EMBL/GenBank = AF179731
<400> 175
Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
1 10 15

Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn 20 25 30

Pro Leu Heu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp 35 40 45

Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu 50 55 60

Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val 65 70 75 80

Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile 85 90 95

Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu 100 105 110

Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe 115 120 125

Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser 130 135 140

Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro 145 150 155 160

Val Leu

<210> 176

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

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<222>			(487			<b></b> .	0.000	tor								
<223> <400>		roau 76	CT =	OII	acto	TÀ T	ecep	LOI							•	
t gtg Val	ace	a at	g tg 1 Cy	t aa s As 5	c cc n Pr	t ct o Le	t ct u Le	c ta u Ty	c ac r Th	r Va	t gc l Al	a at a Me	g ta t Ty	c ca r Gl 15	g agg n Arg	49
1																
ctt t Leu C	gc :ys	tcc Ser	ttg Leu 20	ttg Leu	gtg Val	gct Ala	aca Thr	tca Ser 25	tac Tyr	tgt Cys	tgg Trp	Gly	aga Arg 30	gtc Val	tgt Cys	97
tcc c	ta .	aca	ctt	acc	tac	ttt	cta	ctg	gaa	tta	tcc	ttc	aga	gga	aat	145
Ser I	beu	Thr 35	Leu	Thr	Tyr	Phe	Leu 40	Leu	Glu	Leu	Ser	Phe 45	Arg	Gly	Asn	
aat a	atc	att	aat	aac	ttt	gtc	tgt	gag	cat	gct	gcc	att	gtt	gct	gtg	193
Asn 1	[le 50	Ile	Asn	Asn	Phe	Val 55	Суз	Glu	His	Ala	Ala 60	Ile	Val	Ala	Val	
tct t	tgc	tct	gac	ccc	tat	gtg	agc	cag	gag	atc	act	tta	gtt	tct.	gcc	241
Ser (	Cys	Ser	Asp	Pro	.Tyr	Val	Ser	Gln	Glu	Ile 75	Thr	Leu	Val	Ser	Ala 80	
65					70											
aca t	ttc	aat	gaa	ata	agc	agc	ctg	gtg	atc	act	ctc	act	tcc	tat	gct Ala	289
Thr 1	Phe	Asn	Glu	Ile 85	Ser	Ser	Leu	Val	90	Inr	ьeu	THE	Ser	95	Ala	
ttc a	att	ttt	atc	act	gtc	atg	aag	acg	gct	tcc	att	ggg	ggg	cgc	aag	337
Phe :	Ile	Phe	Ile 100	Thr	Val	Met	Lys	Thr 105	Ala	Ser	Ile	Gly	Gly 110	Arg	Lys	
aaa	gcg	ttc	ttc	acg	tgt	gcc	tcc	cac	ttg	acg	gcc	att	acc	att	ttc	385
Lys .	Ala	Phe 115		Thr	Cys	Ala	Ser 120		Leu	Thr	Ala	11e 125	Thr	Ile	Phe	
cat	ggg	act	att	ctt	ttc	ctc	tac	tgt	gtt	cct	aac	tcc	aaa	agt	tcg	433
His	Gly 130	Thr	Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Ser	Lys	Ser	Ser	•
taa	ctc	atg	gtc	aag	gtg	gcc	tct	gto	ttt	tac	aca	gtg	gto	att	ccc	481
Trp	Leu	Met	Val	Lys	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val	Val	Ile	Pro 160	
145					150					155					100	
atg	ctg															487
Met	Leu															

<210> 177 <211> 162 <212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732

<400> 177

Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg

1 5 10 15

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys 20 25 30

Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn 35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val 50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala 85 90 95

Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
100 105 110

Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe 115 120 125

His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser 130 135 140

Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro 145 150 155 160

Met Leu

<210> 178

<211> 481

<212> DNA

<213> Pan troglodytes

<222> (1) (223> Tax(220> (221> CDS	.(481) luct = ol	factory 1	receptor				ank = AF179733
Leu Ala : 1	le Cys G 5	ln Pro Le	eu Arg T	yr Pro V	al Leu Met	: Asn Gl 15	y Arg
tta tgc aca Leu Cys Th					Ala Gly		
ggg tct ato Gly Ser Ilo 35	c cag gcc Gln Ala	acc ctg Thr Leu	acc ttc Thr Phe 40	cgc ctg Arg Leu	Pro Tyr (	tgt ggg Cys Gly	ccc 145 Pro
aat cag gt Asn Gln Va							
gcc tgt gc Ala Cys Al 65	gac aca Asp Thr	act gtc Thr Val 70	aat gag Asn Glu	ctt gtg Leu Val 75	acc ttt :	gtg gac Val Asp	gtc 241 Val 80
ggg gtg gt Gly Val Va	g gee gee l Ala Ala 85	agt tgc Ser Cys	ttc atg Phe Met	tta att Leu Ile 90	ctg ctc	tcg tat Ser Tyr 95	gcc 289 Ala
aac ata gt Asn Ile Va				Arg Thr	Thr Asp		
cgg gcc tt Arg Ala Ph 11	e Ser Thr	tgt ggc Cys Gly	tcc cac Ser His 120	cta ato Leu Ile	gtg gtc Val Val 125	aca gtc Thr Val	tac 385 Tyr
tat gtc cc Tyr Val Pr 130	c tgt att o Cys Ile	ttc atc Phe Ile 135	Tyr Leu	agg gct Arg Ala	ggc tcc Gly Ser 140	aaa ggc Lys Gly	ccc 433 Pro
ctg gat gg Leu Asp Gl 145	g gcg gcg y Ala Ala	g gct gtg a Ala Val 150	ttt tac Phe Tyr	act gtt Thr Val	. Val Thr	cca tta Pro Leu	ctg 481 Leu 160

<210> 179

<211> 160

<212> PRT

<213> Pan troglodytes

PCT/IB00/02017 WO 01/46262

<220>

<221> misc_feature

<222> (1)..(481)

<223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733

Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg 10

Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His 20

Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro 45 35

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu · 55 50

Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val 75 70 65 ·

Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala 90 95 85

Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His 105 100

Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr 115

Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro 135 130

Leu Asp Gly Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu 155 - 160 150 145

<210> 180

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734

<220>

Va 1	> ( > P > 1 g gc 1 Al	rodu 80 c at a Il	е Су	olf t ca s Hi 5	c cc s Pr	c ct o Le	g ta u Ty	c ta r Ty	r Ar 10	g Va	l Il	e Va	l As	n Pr 15		4	.9
ctc Leu	tgt Cys	ggc Gly	ctg Leu 20	ctg Leu	gtt Val	ctt Leu	gtg Val	tcc Ser 25	tgg Trp	ttc Phe	ctc Leu	agc Ser	ttg Leu 30	tca Ser	tac Tyr	9	7
tcc Ser	ctg Leu	atc Ile 35	cag Gln	agt Ser	ctg Leu	ttg Leu	atg Met 40	ctg Leu	cag Gln	gtg Val	tcc Ser	ttc Phe 45	tgt Cys	acc Thr	agt Ser	14	:5
tgg Trp	gtc Val 50	att Ile	cag Gln	cac His	ttt Phe	tac Tyr 55	tgt Cys	gag Glu	ctt Leu	gct Ala	cag Gln 60	gtc Val	Leu	acg Thr	ctt Leu	19	)3
acc Thr 65	tgc Cys	tca Ser	gac Asp	aca Thr	cac His 70	gtc Val	aat Asn	tac Tyr	atc Ile	ctg Leu 75	ctg Leu	tac Tyr	gtg Val	gtg Val	act Thr 80	24	41
ggc	ctt Leu	ctg Leu	gac Asp	ttt Phe 85	gtg Val	ccc Pro	ttc Phe	tca Ser	gly ggg	atc Ile	ctt Leu	ttc Phe	tcc Ser	tac Tyr 95	acc Thr	28	89
caa Gln	att Ile	gtc Val	tcc Ser 100	Tyr	atc Ile	cta Leu	aga Arg	atc Ile 105	tca Ser	tcc Ser	aca Thr	gat Asp	ggg Gly 110	aaa Lys	cac His	3:	37
aaa Lys	gcc Ala	ttt Phe 115	Ser	acc Thr	tgt Cys	gga Gly	tct Ser 120	cat His	ctg Leu	ttt Phe	gtg Val	gtt Val 125	Ser	tta Leu	ttc Phe	3:	85
tat Tyr	ggg Gly 130	Thr	ggc	ctt Leu	ggt Gly	gtg Val 135	Tyr	ctt Leu	agt Ser	tcc Ser	aat Asn 140	Ala	tcg Ser	tcc Ser	tct Ser	4	33
tcc Ser 145	Trp	tgg Trp	ggc Gly	atg Met	gtg Val	Ala	tcg Ser	gtc Val	atg Met	tac Tyr 155	Thr	gt <u>o</u> Val	gto Val	acc Thr	Pro 160	4	.81
_	ctg Lev															4	187

<210> 181

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature <222> (1)..(487)

<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734

<400> 181

Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg 1 5 10 15

Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser 35 40 45

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 50 55 60

Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr 65 70 75 80

Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr 85 90 95

Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 130 140

Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 182

<211> 487

<212> DNA

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487) <223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735 <220> <221> CDS <222> (2)..(487)<223> Product = olfactory receptor <400> 182 t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys 97 ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt 145 Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe 40 aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att 193 Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt 241 Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly 75 get ttt ata caa ata ecc act tta atg acg atc ata atc tct tat tct. 289 Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser 90 337 cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser 105 100 385 aaa gec tte tee aca tge age gee cat etg ett tet gte tea ttg tae Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr 115 120 tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct 433 Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala .130 135 gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc 481 Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160 487 ctg cta Leu Leu

<210> 183 <211> 162 <212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735

<400> 183

Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15

Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe 35 40 45

Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile 50 55 60

Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly 65 70 . 75 80

Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser 85 90 95

Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr 115 120 125

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140

Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160

Leu Leu

<210> 184

<211> 487

<212> DNA

									.,,							
<213	> Pa	an t	rogl	odyt	es											
<220:	>															
<221:	> m:	isc_	feat	ure												
<222	> (	1)	(487	)												
<223	, m	axon	_ 9	598:	gen	e = :	PTR2	11;	Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF179736
		271011		,	3											
<220:																
<221		DS														
<222			(487													
<223	> P	rođu	ct =	olf	acto	ry r	ecep	tor								
<400	> 1	84														
t at	a ac	c at	t ta	с са	c cc	a ct	g ag	g ta	c ac	a gt	c ct	c at	g aa	c at	c cat	49
Va.	וג ר	a Tl	e Cv	s Hi	s Pr	o Le	u Ar	q Ty	r Th	r Va	l Le	u Me	t As	n Il	e His	
	<b>-</b>	<u> </u>	. 0,	5					. 10					15		
1																
								+	200	++0	a+a	200	act	ato	gat	97
ttc	tgc	ggc	ttg	ctg	att	-	-	2	299	Dha	Wet	Cor	Πh~	Mot	yen geo	
Phe	Суз	Gly	Leu	Leu	TTE	ьeu	ьeu		Arg	PILE	Mec	Ser	1111	Mec	rop	
			20					25					30			
																4.45
gcc	ctg	gtt	cag	agt	ctg	atg	ata	ttt	cag	ctg	tcc	ttc	tgc	aaa	aac	145
Ala	Leu	va1	Gln	Ser	Leu	Met	Ile	Phe	Gln	Leu	Ser	Phe	Cys	Lys	Asn	
		35					40					45				
		•														
			aat	++~	ttc	ttc	tat	gaa	atc	att	cad	atc	atc	aaq	ctc	193
gtt	gaa	alc	500	Tan	Dha	Phe	Cyc	Clu	17-1	1721	Gln	Val	Tle	Tays	Leu	
Val		тте	Pro	ьeu	Pne		Cys	Gru	VOI	Vul	60	144		-1-		
	50					55					60					
																2.41
gcc	tgt	tct	gac	acc	ctc	atc	aac	aac	atc	ctc	ata	tat	דבב	gca	agt	241
Ala	Cys	Ser	Asp	Thr	Leu	Ile	Asn	Asn	Ile	Leu	Ile	Tyr	Phe	Ala	Ser	
65	_				70					75					80	
age	ata	ttt	aat.	σca	att	cct	ctc	tct	gga	ata	att	ttc	tct	tat	tct	289
Cor	Tla	Dho	Glv	λla	Tie	Pro	Len	Ser	Glv	Ile	Ile	Phe	Ser	Tyr	Ser	
Ser	TTE	LIIC	GLY	85					90					95		
				65					,,							
										+ ==	~~~	242	aaa	aarr	tat	337
caa	ata	gtc	acc	tct	gtt	ctg	aga	atg	CCa	Cua	yca	aya	994	Tees	The rese	
Gln	Ile	Val			Val	Leu	Arg			ser	Ala	Arg		пÃ2	TAT	
			100					105					110			
aaa	gcg	ttt	tcc	acc	tgt	ggc	tgt	cac	ctc	tct	gtt	ttt	tcc	ttg	ttc	385
Lvs	Ala	Phe	Ser	Thr	Cys	Gly	Cys	His	Leu	Ser	Val	Phe	Ser	Leu	Phe	
-3.5		115				_										
h h			~~+	+++	aaa	gtg	tcc	att	agt	tet	act	att	act	gag	tct	433
tat	999	aca	get	77-	999	949	Cor	T10	Cor	Cor	λla	17a 1	Δla	Glu	Ser	
Tyr			Ala	Pne	GLY			116	Ser	Ser	140	· val	2124		Ser	
	130					135					140					
																401
tcc	cga	att	act	gct	gtg	ggt	tca	gtg	atg	tac	act	gtg	gto	сса	caa	481
Ser	Arq	Ile	Thr	· Ala	Val	Gly	Ser	Val	. Met	Tyr	Thr	Val	Val	Pro	Gln	
145					150					155					160	
~ t-~	+ -															487
_	atg															
wet	Met															

Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn 35 40 45

Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu 50 55 60

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser 65 70 75 80

Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser 85 90 95

Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe 115 120 125

Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser 130 135 140

Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln 145 150 155 160

Met Met

**	0 01/	10202							195							
<210	> 1:	86														
<211:		87														
<212		NA.														
<213			rogl	odvt.	es											
<220								•								
<221		isc	feat	ure										•		
<222			(487													
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<220				,	5											
<221		DS														
<222			(487	')												
<223	-	-			acto	ry r	ecep	tor								
<400		86				-										
		c at	a tg	ıt ca	c cc	t ct	сса	c ta	c ac	t gt	c at	c at	g ag	g ga	a gag	49
Va	l Āl	a Il	e Cy	rs Hi	s Pr	o Le	u Hi	s Ty	r Th	r Va	1 Il	e Me	t Ar	g G1	u Glu	
1			_	5					10					15		
ctc	tgt	gtc	ttc	tta	gtg	gct	gta	tct	tgg	att	ctg	tct	tgt	gcc	agc	97
Leu	Cys	Val	Phe	Leu	Val	Ala	Val	Ser	Trp	Ile	Leu	Ser	Суѕ	Ala	Ser	
			20					25					30			
tcc	ctc	tct	cac	acc	ctt	ctc	ctg	acc	cgg	ctg	tct	ttc	tgt	gct	gcg	145
Ser	Leu	Ser	His	Thr	Leu	Leu		Thr	Arg	Leu	Ser		Cys	Ala	Ala	
		35					40					45				
																193
aac	acc	atc	CCC	cat	gtc	ttc	tgt	gac	CEE	gct	gcc	ctg	CEC	aag	ton	193
Asn		Ile	Pro	His	Val		Cys	Asp	Leu	ATA		rea	ьец	пуs	пеп	
	50					55					60					
<b>.</b>	<b></b>	<b>.</b>	+	250	ttc	ata	<del>-</del>	a=a	ctc	ata	ato	ttc	aca	αta	aaa	241
Com	Cura	Cox	yac Nan	Tla	Phe	T.011	Acn	Glu	Len	Val	Met	Phe	Thr	Val	Glv	
65	Cys	ser	ASD	TTE	70	пси	non	0		75					80	
03					, 0											
ata	ata	atc	att	acc	ctg	cca	ttc	atq	tat	atc	ctg	gta	tca	tat	ggc	289
Val	Val	Val	Ile	Thr	Leu	Pro	Phe	Met	Cys	Ile	Leu	Val	Ser	Tyr	Gly	
• • • •				85					90					95		
tac	att	ggg	gcc	acc	atc	ctg	agg	gtc	cct	tca	acc	aaa	ggg	atc	cac	337
Tyr	Ile	Gly	Ala	Thr	Ile	Leu	Arg	Val	Pro	Ser	Thr	Lys	Gly	Ile	His	
•		_	100					105					110			
aaa	gca	ttg	tcc	aca	tgt	ggc	tcc	cat	ctc	tct	gtg	gtg	tct	ctc	tat	385
Lys	Ala	Leu	Ser	Thr	Cys	Gly			Leu	Ser	Val		Ser	Leu	Tyr	
		115					120					125				
														_		422
					ggc											433
Tyr	Gly	Ser	Ile	Phe	Gly			Leu	Phe	Pro		Val	Ser	Ser	Ser	
	130					135					140					
										_						481
					att											#OT
	Asp	Lys	Asp	val	Ile		Ala	ьeu	met			val	val	THE		
145					150					155					160	
<u></u>	<u>.</u>															487
atg	ttg															

Met Leu

<210> 187 <211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR212; Accession DDBJ/EMBL/GenBank = AF179737

<400> 187

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 40

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 188 <211> 484 <212> DNA <213> Hylobates lar <220> <221> misc_feature <222> (1)..(484) <223> Taxon = 9580; gene = HLA121; pseudogene; Accession DDBJ/EMBL/GenBank = AF179738 <400> 188 tgtggctatc tgcctgccgc ttaggtatcc agagctcatg agtgggcaga cctgcatgca 60 gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccatccttgt 120 ctggcgcctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc 180 agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tggtggccac 240 agetgteetg acactggeec ecetettget catetgeetg tettacettt teatettgte 300 tgccatcctt agggtaccct ctgctgcagg ccggcgcaaa gccttctcca cctgctcagc ccacctcaca gtggtggtgg ttttttaagg gacaatttcc ttcatgtact tcaaacccaa ggccaaggac cccaacgtgg ataagattgt tgcattgttg tatggggttg tgacaccctc 484 gctg <210> 189 <211> 487 <212> DNA <213> Hylobates lar <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739 <220> <221> CDS <222> (2)..(487) <223> Product = olfactory receptor <400> 189 t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tcc cag agg Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys 25

ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat

145

Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn

aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
50 55 60

tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala

65 70 75 80

aca ttc aat gaa ata agc agt ctg atg atg att ttc act tcc tat gct

Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala

85

90

95

ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag

Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys

100 105 110

aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc

125

126

127

128

128

129

125

cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca

433

His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser

130

135

140

tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc

Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro

145

150

160

atg gtg 487
Met Val

<210> 190

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

<400> 190

Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg 1 5 10 15

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
20 25 30

Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn

45

40

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val 50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala 85 90 90

Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe 115 120 125

His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser 130

Met Val

<210> 191

<211> 486

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(486)

35

<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 191

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

97

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

25 30 20

gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cag Gln	ctt Leu	tcc Ser	ttt Phe 45	tgt Cys	gct Ala	gac Asp		145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu		193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	ttg Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ttg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly		289
cac His	att Ile	ggg Gly	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tct Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	Thr	atc Ile	tat Tyr		385
tat Tyr	ggg Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr	٠	433
aat Asn 145	Asp	aag Lys	aac Asn	ata Ile	att Ile 150	Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	Thr	gta Val	gtc Val	act Thr	ccc Pro 160		481
atg Met																	486

<210> 192

<211> 161

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(486)
<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740
<400> 192

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 5 10 1

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160

Met

<210> 193

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

49

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 193

t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg
Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg

1 5 10 15

					gct Ala									97
-			_		aca Thr									145
	_	_			ttc Phe	_	_	_						193
					gca Ala 70									241
					atc Ile									289
		_	_	_	atc Ile	_			_	_		-		337
					tgt Cys									385
					ctc Leu									433
					ctg Leu 150									481
_	ttg Leu													487

<210> 194

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)
<223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<400> 194

Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg 5 10

Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val 20 25 30

Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr 35 40 45

Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu 50 55 60

Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr 65 70 75 80

Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr 85 90 95

His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe 115 120 125

Tyr Ile Ser Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser 130 135 140

Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 195

<211> 487

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 195

W	O 01	/4626	2						204						PC1/III	00/02017
t gtg Val	g gc L Al	c at a Il	c tg e Cy	c aa s Ly 5	g cc s Pr	t ct o Le	g ca u Hi	t ta s Ty	c tt r Le 10	u As	t at n Il	c at e Me	g aa t As	t cg n Ar 15	a aga g Arg	49
gtc i Val (	tgc Cys	ata Ile	ctg Leu 20	ctt Leu	gtt Val	ttt Phe	act Thr	tct Ser 25	tgg Trp	ctg Leu	att Ile	tca Ser	ttc Phe 30	tta Leu	atc Ile	97
ata 1	ttc Phe	cct Pro 35	gca Ala	ctc Leu	atg Met	ttg Leu	ctc Leu 40	tta Leu	aag Lys	ctt Leu	gat Asp	tac Tyr 45	tgt Cys	agg Arg	tct Ser	145
aat Asn	att Ile 50	att Ile	gac Asp	cat His	ttt Phe	acc Thr 55	tgt Cys	gat Asp	tat Tyr	ttt Phe	ccc Pro 60	ctg Leu	ctg Leu	caa Gln	ctt Leu	193
gct Ala 65	tgt Cys	tca Ser	gac Asp	aca Thr	aaa Lys 70	ttc Phe	tta Leu	gag Glu	gtg Val	atg Met 75	gca Ala	ttt Phe	tct Ser	tgt Cys	gct Ala 80	241
gtg Val	ttt Phe	act Thr	cta Leu	atg Met 85	ttc Phe	act Thr	ttg Leu	gca Ala	tta Leu 90	ata Ile	tct Ser	ctg Leu	tcc Ser	tac Tyr 95	ata Ile	289
Tyr	Ile	Ile	Arg 100	Thr	Ile	ttg Leu	Arg	Ile 105	Pro	Ser	Thr	Ser	Gln 110	Arg	Thr	337
Lys	Ala	Phe 115	Ser	Thr	Cys	tct Ser	Ser 120	His	Met	Val	Val	11e 125	Ser	Ile	Ser	385
Tyr	Gly 130	Ser	Cys	Ile	Phe	Met 135	Tyr	Ile	Lys	Pro	Ser 140	Ala	Lys	Asp	aga Arg	433
gtg Val 145	tcc Ser	ttg Lev	ago Ser	aag Lys	gga Gly 150	val	gca	ata Ile	cta Leu	aac Asn 155	Thr	tca Ser	gta Val	gcc Ala	Pro 160	481
-	atg Met															487
<21 <21 <21 <21	1> 2>	196 162 PRT Hyle	obate	es la	ar											

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<211> 162
<212> PRT
<213> Hylobates lar
<220>
<221> misc_feature
<222> (1)..(487) <223> Taxon = 9580; gene = HLA125; Accession
DDBJ/EMBL/GenBank = AF179742
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<400> 196

Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg

5 10

Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile

Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser 40 45

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr 105 100

Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser 120

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 135

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro 145 150 155

Met Met

<210> 197

<211> 484

<212> DNA

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(484) <223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743

<220>

<221> CDS

<222: <223: <400:	> P > 1	rođu 97	(484 ct =	olf												49
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ctc Leu	tgt Cys	gtc Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	ata Ile	tct Ser 25	tgg Trp	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97
tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	ctt Leu	ctc Leu	ctg Leu 40	acc Thr	cgg Arg	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala	145
Asn	acc Thr 50	atc Ile	ccc Pro	cac His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 ggg	241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc	289
tac Tyr	att Ile	gjå aaa	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	ggg Gly 110	atc Ile	cac His	337
aaa Lys	gcg Ala	tcc Ser 115	acg Thr	tgt Cys	ggc Gly	tcc Ser	cat His 120	ctt Leu	tct Ser	gtg Val	gtg Val	tct Ser 125	ctc Leu	tat Tyr	tat Tyr	385
Gly ggg	tca Ser 130	Ile	ttt Phe	ggc Gly	cag Gln	tac Tyr 135	ctt Leu	ttc Phe	ccg Pro	acc	gca Ala 140	agc Ser	agt Ser	tcc Ser	att Ile	433
gac Asp 145	aag Lys	gat Asp	gtc Val	att Ile	gtg Val 150	gct Ala	gtc Val	atg Met	tac Tyr	aca Thr 155	gtg Val	atc Ile	aca Thr	ccc Pro	atg Met 160	481
ttg Leu														٠		484

<210> 198

<211> 161

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(484)
<223> Taxon = 9580; gene = HLA126; Accession DDBJ/EMBL/GenBank = AF179743
<400> 198
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

Leu Cys Val Phe Leu Val Ala Ile Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 160

Leu

<210> 199
<211> 487
<212> DNA
<213> Hylobates lar
<220>
<221> misc_feature

<222> (1)..(487)

	-								208							
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<221:		DS														
<222			(487 ct =		acto	רייני די	ecen	tor								
<223: <400:	> 1	99														
t at	a ac	c at	c tg e Cy	t ca s Hi 5	c cc s Pr	t ct o Le	a ca u Hi	t ta s Ty	t go r Al 10	a Th	c at r Il	c at e Me	g ag t Se	t ca r Gl 15	g agc n Ser	49
cag	+~+	at a	ato	cta	ata	act	aaa	tcc	taa	gtc	atc	gct	tgt	gcg	tgt	97
Gln	Cys	Val	Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys	
act	ctt	tta	cat	acc	ctc	ctc	cta	qcc	cag	ctt	tcc	ttt	tgt	gct	gac	145
Ala	Leu	Leu 35	His	Thr	Leu	Leu	Leu 40	Ala	Gln	Leu	Ser	Phe 45	Cys	Ala	Asp	
a24	a+c	atc	cct	cac	ttc	ttc	tat	gac	ctt	ggt	gcc	ctg	ctc	aag	ttg	193
His	Ile 50	Ile	Pro	His	Phe	Phe 55	Cys	Āsp	Leu	Gly	Ala 60	Leu	Leu	Lys	Leu	
	+	+ ==	~at	acc	tcc	ctc	aat	caq	tta	gca	atc	ttt	aca	gca	gga	241
Ser	Cys	Ser	Asp	Thr	Ser	Leu	Asn	Gln	Leu	Ala	Ile	Phe	Thr	Ala	GIA	
65					70					75					80	
++a	aca	acc	att	atσ	ctt	cca	ttc	ttg	tgc	atc	ctg	gtt	tct	tat	ggt	289
Leu	Thr	Ala	Ile	Met 85	Leu	Pro	Phe	Leu	Суs 90	Ile	Leu	Val	Ser	Tyr 95	Gly	
		~~~	ata	200	atc	ctc	cag	att	ccc	tct	acc	aaq	aac	ata	tgc	337
His	Ile	Gly	Val 100	Thr	Ile	Leu	Gln	Ile 105	Pro	Ser	Thr	Lys	Gly 110	Ile	Cys	
		1 - 1	.		- ~+	~~3	tac	cac	ctc	tca	ata	ata	act	atc	tat	385
aaa Lvs	gcc Ala	Leu	Ser	Ile	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Thr	Ile	Tyr	
-4-		115					120					125				
tat	aaa	aca	att	att	aat	ctc	tat	ttt	ctt	ccc	cca	tcc	agc	aac	acc	433
Tyr	Gly 130	Thr	Ile	Ile	Gly	Leu 135	Tyr	Phe	Leu	Pro	Pro 140	Ser	Ser	Asn	Thr	
														200		481
aat	gac	aag	aac	ata Tle	att	gct Ala	. tca Ser	gtg Val	ata Il ϵ	TVI	aca Thr	. yca · Val	. y.c	Thr	Pro	#0#
145		пўз	ASII	. 116	150			, , ,		155				•	160	
	ttg						•									487
Met	Leu	•														

<210> 200

<211> 162

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744

<400> 200

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 40

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 · 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 201

<211> 484

<212> DNA

<213> Hylobates lar

<220><221><222><222><223><220><221><222><4000t gt	m (:	l) axon DS 2) rodu 01	(484 ct =) 580;) olf	acto c cc	ry r t ct	ecep c ca	tor c ta	c ac	t gt	c at	c at	g ag	g ga	ank = a gag u Glu	AF179745
1	I AI	9 TT	есу	5	2 F.	O DC	u	J .,	10					15		
ctc Leu	tgt Cys	gtc Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	tgg Trp	att Ile	ctg Leu	Ser	tgt Cys 30	gcc Ala	agc Ser	97
tcc Ser	ctc Leu	tct Ser 35	cac His	acc Thr	ctt Leu	ctc Leu	ctg Leu 40	acc Thr	cgg Arg	ctg Leu	tct Ser	ttc Phe 45	tgt Cys	gct Ala	gcg Ala	145
aac Asn	acc Thr 50	atc Ile	ccc Pro	cac His	gtc Val	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	gct Ala	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	atc Ile	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJA āāā	241
gtg Val	gtg Val	gtc Val	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289
tac Tyr	att Ile	Gly	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	ggg Gly 110	atc Ile	cac His	337
aaa Lys	gcg Ala	tcc Ser 115	acg Thr	tgt Cys	ggc Gly	tcc Ser	cat His 120	Leu	tct Ser	gtg Val	gtg Val	tct Ser 125	ctc Leu	tat Tyr	tat Tyr	385
Gly aga	tca Ser 130	Ile	ttt Phe	ggc	cag Gln	tac Tyr 135	Leu	ttc Phe	ccg Pro	acc	gca Ala 140	Ser	agt Ser	tcc Ser	att Ile	433
gac Asp 145	Lys	gat Asr	gtc Val	att	gtg Val	. Ala	gto Val	atg Met	tac Tyr	aca Thr	· Val	ato Ile	aca Thr	ccc Pro	atg Met 160	481
ttg Leu																484

<210> 202 <211> 161

<212> PRT

<213> Hylobates lar

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank AF179745

<400> 202

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu 1 5 10 15

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 40

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 145 150 155 160

Leu

<223> <400>	mis (1) Tax CDS (2 Pro 20)	A loba sc_i) xon S) odu	(484 ct = c ta	ure) 580;) olf	acto c cc	ry r	ecep a ca	tor t ta	t gc	c ac	c at	c at	g ag	t ca	g agc n Ser	AF179746 49
1 cag to			- • -	5		~a+	~~~	taa	10		atc	act	tat	15 aca		97
Gln Cy	gt g ys V	al	atg Met 20	Leu	Val	Ala	Gly	Ser 25	Trp	Val	Ile	Ala	Cys 30	Ala	Cys	•
gct ct Ala Le	eu L	tg eu 5	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cag Gln	ctt Leu	tcc Ser	ttt Phe 45	tgt Cys	gct Ala	gac Asp	145
cac at His I	le I	tc le	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu	193
tcc to Ser Co	gc t ys S	ca Ser	gat Asp	acc Thr	ttc Phe 70	ctc Leu	aat Asn	gag Glu	ctg Leu	gtc Val 75	atg Met	ttc Phe	aca Thr	gta Val	80 GJA aaa	241
gtg g Val V	tg g al V	gtc /al	att Ile	acc Thr 85	ctg Leu	cca Pro	ttc Phe	atg Met	tgt Cys 90	atc Ile	ctg Leu	gta Val	tca Ser	tat Tyr 95	ggc Gly	289
tac a Tyr I	tt g le (ggg	gcc Ala 100	acc Thr	atc Ile	ctg Leu	agg Arg	gtc Val 105	cct Pro	tca Ser	acc Thr	aaa Lys	ggg Gly 110	atc Ile	cac His	337
aaa g Lys A	la s	tcc Ser 115	acg Thr	tgt Cys	ggc	tcc Ser	cat His 120	Leu	tct Ser	gtg Val	gtg Val	tct Ser 125	Leu	tat Tyr	tat Tyr	385
ggg t Gly S 1	ca ser :	ata Ile	ttt Phe	ggc	cag Gln	tac Tyr 135	Leu	ttc Phe	ccg Pro	acc Thr	gca Ala 140	Ser	agt Ser	tcc Ser	att Ile	433
gac a Asp I 145	ag i	gat Asp	gtc Val	att Ile	gtg Val 150	Ala	gtc Val	atg Met	tac Tyr	aca Thr 155	Val	atc Ile	aca Thr	ccc Pro	atg Met 160	481
ttg Leu													•			484

213

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 40

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 55 50

Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 75 65

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 90 85

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His 105 100

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr 115 120

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile 135 130

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met 155 150 145 .

Leu

WO 01/46262 PCT/IB00/02017

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<211> 486
<212> DNA
<213> Hylobates lar
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                                                                     120
gcccagcttt ccttttgtgc tgaccacatc atccctcact tcttctgtga ccttggtgcc
                                                                     180
ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga
                                                                     240
ttgacagcca ttatgcttcc attcttgtgc atcctggttt cttatggtca cattggggtc
                                                                     300
accatectee agatteeete taccaaggge atatgeaaag eettgteeat ttgtggatee
                                                                     360
caccteteag tggtgactat ctattatggg acaattattg gtetetattt tetteececa
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tccagcaaca ccaatgacaa gaacataatt gcttcagtga tatacacagt agtcactccc
                                                                     480
                                                                     486
atgttg
<210> 206
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<222>
       (2)..(487)
<223> Product = olfactory receptor
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  Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
                                       10
                   5
                                                                       97
 ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac
 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
                                                     30
                                 25
             20
 tcc ctg atc cag agt ctg ttg atg ctg cgg gtg tcc ttc tgc acc agt
                                                                      145
 Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
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tgg gtc Trp Val 50	att Ile	cag Gln	cac His	ttt Phe	tac Tyr 55	tgt Cys	gag Glu	ctt Leu	gct Ala	cag Gln 60	gtc Val	ctc Leu	acg Thr	ctt Leu	193.	
gcc tgc Ala Cys 65	tca Ser	gac Asp	aca Thr	cac His 70	atc Ile	aat Asn	tac Tyr	atc Ile	ctg Leu 75	ctc Leu	tac Tyr	atg Met	gtg Val	acc Thr 80	241	
ggc ctt Gly Leu	ttg Leu	ggc Gly	ttt Phe 85	gtg Val	ccc Pro	ttc Phe	tca Ser	90 90	atc Ile	ctt Leu	ttc Phe	tcc Ser	tac Tyr 95	acc Thr	289	
caa atc Gln Ile	gtc Val	tcc Ser 100	tcc Ser	atc Ile	ctg Leu	aga Arg	atc Ile 105	tca Ser	tcc Ser	cca Pro	gat Asp	ggg Gly 110	aaa Lys	cac His	337	
aaa gcc Lys Ala	ttt Phe 115	Ser	acc Thr	tgt Cys	gga Gly	tct Ser 120	cat His	ctg Leu	tct Ser	gtg Val	gtt Val 125	tct Ser	tta Leu	ttc Phe	385	
tat ggg Tyr Gly 130	Thr	ggt	ctt Leu	ggc	gtg Val 135	tat Tyr	ctt Leu	agt Ser	tcc Ser	aat Asn 140	Ala	tcg Ser	tcc Ser	tct Ser	433	
tcc tgg Ser Trg 145	cgg Arg	ggc Gly	atg Met	gtg Val 150	Ala	tcg Ser	gta Val	atg Met	tac Tyr 155	Thr	gtg Val	gta Val	acc	ccc Pro 160	481	
aat gtg Asn Val															487	

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<213> Hylobates lar

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Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr 25 20

Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser 40

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu 50 . 55 60 Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr 75 70 Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr 90 Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His 105 100 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 125 Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser 135 140 Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 150 155 Asn Val <210> 208 <211> 487 <212> DNA <213> Hylobates lar <220>

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gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctc Leu	ctg Leu 40	gcc Ala	cag Gln	ctt Leu	tcc Ser	ttt Phe 45	tgt Cys	gct Ala	gac Asp		145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu		193
tcc Ser 65	tgc Cys	tca Ser	gat Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	ttg Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80		241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ttg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly	V.	289
cac His	att Ile	GJÀ aaa	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	act Thr 105	ccc Pro	tct Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys		337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	att Ile	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr		385
tat Tyr	ggg Gly 130	aca Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	tcc Ser	agc Ser	aac Asn	acc Thr		433
aat Asn 145	Asp	aag Lys	aac Asn	ata Ile	att Ile 150	gct Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	ccc Pro 160	•	481
_	ttg Leu																487
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			Cys	His 5	Pro	Leu	His	: Туг	Ala 10	Thr	·Ile	Met	: Ser	15	Ser		

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 , 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

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Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
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W O 01/40202		21	19	101,1200,0201.
acc tgc att caa Thr Cys Ile Gln 20	ctg gca gtt Leu Ala Val	att tct tgg Ile Ser Trg 25	g too agt ago to Ser Ser Ser Pl 30	ne Leu Cys
tcc atg gtt atc Ser Met Val Ile 35	aat gtt ctc Asn Val Leu	acg ttg agt Thr Leu Ser 40	ttg ccc tac to Leu Pro Tyr Cy 45	gt ggg cct 145 ys Gly Pro
aat atc ctg aat Asn Ile Leu Asn 50	cac ttt ttc His Phe Phe 55	tgt gag gta Cys Glu Val	a cct act gtc c l Pro Thr Val L 60	tg agg ttg 193 eu Arg Leu
tct tgc acc gac Ser Cys Thr Asp 65	acc tca ttc Thr Ser Phe 70	acg gag ctg Thr Glu Let	g gtt gtt ttt a u Val Val Phe I 75	tc ttc agt 241 le Phe Ser 80
atc atc att gtc Ile Ile Ile Val	ttc atc cct Phe Ile Pro 85	ttc ctc ctc Phe Leu Ler 90	c att gtt gtt t u Ile Val Val S	cc tat gtc 289 er Tyr Val 95
cgg atc ctt caa Arg Ile Leu Gln 100	Ser Val Leu	agg atg cg Arg Met Ar 105	g Ser Ala Ser G	gg cgg tat · 337 ly Arg Tyr 10
aag gca tta tcc Lys Ala Leu Ser 115	acc tgt acc Thr Cys Thr	tcc cat tt Ser His Le 120	g aca gtg gta a u Thr Val Val T 125	cc tta ttt 385 hr Leu Phe
tat ggg act gcc Tyr Gly Thr Ala 130	atc ctc atg Ile Leu Met 135	Tyr Met Ar	a cca cag tcg a g Pro Gln Ser A 140	gg tct tcc 433 org Ser Ser
tgg gct ggc ggc Trp Ala Gly Gly 145	aag atc att Lys Ile Ile 150	geg gtt tte Ala Val Ph	c tac acg gtg g e Tyr Thr Val V 155	rtc aca ccc 481 Val Thr Pro 160
atg ctt Met Leu				487
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Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys 25 20

Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro 45

Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu 55

Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser 75 70

Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val . 90 85

Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr 105

Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe 120

Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser 135 130

Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro 155 145 150

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<211> 488

<212> DNA

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<220>

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		attasaas	anntnaa	cca tttct	tctat c	agatocta	t 180
taatgaattt cccct	actgt gg	Cccyayya	aggegaa	cca cccc	scouge g	,49409004	
ccttgttgaa gctg	cctgt gt	agacacat	ccctgtt	tga gaagg	gtgata t	ttgcttgc	t 240
gtgtcttcat gctt	tette ce	attctcca	tcatcgt	ggc ctcci	tatgct o	gcattcta	g 300
ggactgtgct gcaa	tgcac to	tgctcagg	cctggaa	aaa ggcc	ctggcc a	ectgctcc	t 360
cccacctgac agct	jtcacc ct	cttctatg	gggcagc	cat gttc	atctac o	tgaggcct	a 420
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ccatgctg							488 ·
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Phe Cys Val Phe	Leu Val	Ala Val	Ser Trp 25 acc cag	Ile Leu	Ser Cys 30 ttc tgt	Ala Ser	97 145
Phe Cys Val Phe 20 tcc ctc tct cac Ser Leu Ser His	Leu Val	ctc ctg Leu Leu 40	Ser Trp 25 acc cag Thr Gln gac ctt	ctg tct Leu Ser	Ser Cys 30 ttc tgt Phe Cys 45 ctg ctc	Ala Ser gct gcg Ala Ala	97 145 193
Phe Cys Val Phe 20 tcc ctc tct cac Ser Leu Ser His 35 aac acc atc ccc Asn Thr Ile Pro	Leu Val	Ala Val ctc ctg Leu Leu 40 ttc tgt Phe Cys 55 ctc aat	Ser Trp 25 acc cag Thr Gln gac ctt Asp Leu gag ctg	ctg tct Leu Ser gct gcc Ala Ala 60 gtc atg	Ser Cys 30 ttc tgt Phe Cys 45 ctg ctc Leu Leu ttc aca	Ala Ser gct gcg Ala Ala ag ctg Lys Leu gta ggg	97 145 193
Phe Cys Val Phe 20 tcc ctc tct cac Ser Leu Ser His 35 aac acc atc ccc Asn Thr Ile Pro 50 tcc tgc tca ga Ser Cys Ser As	Leu Val acc gtt Thr Val cat gtc His Val atc ttc	ctc ctg Leu Leu 40 ttc tgt Phe Cys 55 ctc aat Leu Asn	Ser Trp 25 acc cag Thr Gln gac ctt Asp Leu gag ctg Glu Leu atg tgt	ctg tct Leu Ser gct gcc Ala Ala 60 gtc atg Val Met 75 atc ctg	Ser Cys 30 ttc tgt Phe Cys 45 ctg ctc Leu Leu ttc aca Phe Thr	Ala Ser gct gcg Ala Ala agg ctg Lys Leu gta ggg Val Gly 80	97 145 193 241

WO 01/4	6262					222						PCT/I	B00/02017
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aaa gca t Lys Ala L	tg tcc eu Ser .15	aca tg	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr	385
tat ggg t Tyr Gly S 130	ca ata Ser Ile	ttt gg Phe Gl	c cag Gln 135	tac Tyr	ctt Leu	ttc Phe	ccg Pro	act Thr 140	gta Val	agc Ser	agt Ser	ttt Phe	433
att gac a Ile Asp I 145	ag gat Ys Asp	gtc at Val I1 15	e Val	gct Ala	ctc Leu	atg Met	tac Tyr 155	acg Thr	gtg Val	gtc Val	aca Thr	ccc Pro 160	481
acg ttg Thr Leu													487
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Phe Cys	Val Phe 20	e Leu Va	al Ala	a Val	. Ser 25	Trp	Ile	. Leu	. Ser	Cys 30	Ala	Ser	

Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His

110

105 100

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 120 115

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe 140 · 130 135

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 155 150

Thr Leu

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<221> misc_feature

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									225	•							
gga Gly	ctg Leu	tct Ser	tgc Cys	act Thr 85	att Ile	gtg Val	ttt Phe	ctg Leu	ctc Leu 90	tta Leu	ctc Leu	atc Ile	tct Ser	tat Tyr 95	ggt Gly		289
			cac His 100														337
gcc Ala	ctc Leu	tca Ser 115	acc Thr	tgc Cys	agt Ser	tcc Ser	cac His 120	atc Ile	act Thr	gtg Val	gtt Val	gtc Val 125	ttc Phe	ttc Phe	ttt Phe		385
			att Ile														433
gac Asp 145	aaa Lys	tca Ser	gtg Val	agt Ser	gtg Val 150	ttt Phe	tat Tyr	aca Thr	gtc Val	ata Ile 155	acc Thr	cca Pro	atg Met	ct			477
	L> 3 2> 1 3> 0	218 L58 PRT Gori	lla g	gori.	lla												
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Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys 105 100 Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe 120 Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile 135 130 Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met 150 <210> 219 <211> 488 <212> DNA <213> Gorilla gorilla <220> <221> misc_feature <222> (1)..(488) <223> Taxon = 9593; gene = GGO107; Accession DDBJ/EMBL/GenBank = AF179756 <221> CDS <222> (2)..(487) <223> Product = olfactory receptor t ctt gcc atc tgc tat cct tta cac tac gga gcc atg atg agt agc ctg Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly Ala Met Met Ser Ser Leu 5 1 97 ctc tca gtg cag ttg gcc ctg ggc tcc tgg gtt tgt ggt ttc atg gcc Leu Ser Val Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Met Ala 25 20 att gca gtg ccc aca gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc 145 Ile Ala Val Pro Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro 35 cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg 193 Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu 55 50 241 gcc tgc acc aac aca cag gca gta gag ctt gtg gcc ttt gtg att gct Ala Cys Thr Asn Thr Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala gtt gtg gtt atc ctg agt tca tgc ctc atc acc ctt gtc tcc tat gtg 289 Val Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val 95 85

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tac Tyr	atc Ile	atc Ile	agc Ser 100	acc Thr	atc Ile	ctc Leu	agg Arg	atc Ile 105	ccc Pro	tct Ser	gcc Ala	agt Ser	ggc Gly 110	cgg Arg	agc Ser	337
aaa Lys	gcc Ala	ttc Phe 115	tcc Ser	acg Thr	tgc Cys	tcc Ser	tcg Ser 120	cat His	ctc Leu	acc Thr	gtg Val	gtg Val 125	ctc Leu	att Ile	tgg Trp	385
tat Tyr	ggg Gly 130	tcc Ser	aca Thr	aťt Ile	ttc Phe	ctt Leu 135	cac His	gtc Val	cgc Arg	acc Thr	tct Ser 140	atc Ile	aaa Lys	gac Asp	gcc Ala	433
ttg Leu 145	gat Asp	ctg Leu	atc Ile	aaa Lys	gct Ala 150	gtc Val	cac His	gtc Val	ctg Leu	aac Asn 155	act Thr	gtg Val	gtg Val	act Thr	cca Pro 160	481
-	tta Leu															488
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<40 Leu 1	0> Ala	220 Ile		Tyr 5	Pro	Leu	His	Tyr	Gly 10	Ala	Met	Met	Ser	Ser 15	Leu	AF179756
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Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
115 120 125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala 130 135 140

Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro 145 150 155 160

Val Leu

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<211> 487

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<213> Gorilla gorilla

<220>

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cag	tgt	gtc	atg Met	ctg	gtg	gct	ggg	tcc	tgg	gtc Val	atc	gct	tgt Cvs	gcg	tgt Cvs	97
Gin	cys	vaı	20	ьеи	vai	ALG	GIĀ	25	пр	Val	116	nia	30	niu	CYD	
gct	ctt	ttg	cat	acc	ctc	ctc	ctg	gcc	cgg	ctt	tcc	ttc	tgt	gct	gac	145
Ala	Leu	Leu 35	His	Thr	Leu	ren	ьеи 40	Ala	Arg	ьец	ser	45	cys	мта	Asp	
cac	atc	atc	cct	cac	ttc	ttc	tgt	gac	ctt	ggt	gcc	ctg	ctc	aag	ttg	193
His	Ile 50	Ile	Pro	His	Phe	Phe 55	Cys	Asp	Leu	GIĀ	Ala 60	Leu	Leu	гăг	ьеи	
tcc	tgc	tca	gac	acc	tcc	ctc	aat	cag	tta	gca	atc	ttt	aca	gca	gga	241
Ser 65	Cys	Ser	Asp	Thr	Ser 70	Leu	Asn	Gln	Leu	Ala 75	Ile	Phe	Thr	Ala	80 Gly	
ttg	aca	gcc	att	atg	ctt	cca	ttc	ctg	tgc	atc	ctg	gtt	tct	tat	ggt	289
Leu	Thr	Ala	Ile	Met 85	Leu	Pro	Phe	Leu	Cys 90	Ile	Leu	Val	Ser	Tyr 95	GlĀ	
cac	att	ggg	gtc	acc	atc	ctc	cag	att	CCC	tct	acc	aag	ggc	ata	tgc	337
His	Ile	Gly	Val 100	Thr	Ile	Leu	Gln	11e 105	Pro	Ser	Thr	гÀ2	110	TIE	Cys	
aaa	gcc	ttg	tcc	act	tgt	gga	tcc	cac	ctc	tca	gtg	gtg	act	atc	tat	385
Lys	Ala	Leu 115	Ser	Thr	Cys	GIĀ	120	HIS	ьeu	Ser	vai	125	THE	TTE	TÄT	
			att													433
Tyr	Gly 130	Thr	Ile	IIe	GIĀ	135		Pne	ьeu	PIO	140		per	ASII	1111	
aat	gac	aag	aac	ata	att	gct	tca	gtg	ata	tac	aca	gta	gtc	act	CCC	481
Asn 145		Lys	Asn	Ile	11e 150		ser	val	TTE	1yr 155		val	val	rnr	Pro 160	
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Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 150

Met Leu

<210> 224

<211> 487

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<223>		noxe	= 9	606;	gen	e = 1	HSAI	; AC	cess	lon	טשטט	/ EMB	п/се	IIDaii	к - м	F1797	J 9
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t gta Val	Al:	a Ile	a cy e Cv	c aa s As	n Pr	o Le	u Le	u Ty	r Pr	o Va	l Me	t Me	t Se	r As	n Lys		
1				5					10					15	i		
					,			L		~+~		~~+	++0	ctc	cat		97
ctc a	igc (gct Nla	cag	ttg	Cta	agt Ser	Ile	Ser	Tvr	yca Val	Ile	Gly	Phe	Leu	His		٠.
neu s	er .		20	<u> L</u> Cu	Dea	502		25	-4-			•	30				
																1	4 E
cct c	tg	gtt	cat	gtg	agt	tta	cta	ttg	cga	Cta	Thr	Phe	Cvs	agg	Phe	1.	45
Pro 1		vai 35	HIS.	vaı	ser	пеп	40	neu	Arg	пец		45	0,2	5			
																_	
aac a	ata	ata	cat	tat	ttc	tac	tgt	gaa	att	tta	caa	ctg	ttc	aaa	att	1	.93
Asn I		Ile	His	Tyr	Phe	Tyr 55	Cys	GIU	TTE	ьeu	60	ьец	Pne	ъys	TIE		
-	50					33											
tca t	tgc	aat	ggt	cca	tct	atţ	aac	gca	cta	ata	ata	ttt	att	ttt	ggt	. 2	41
Ser (Cys	Asn	Gly	Pro		Ile	Asn	Ala	Leu	Ile 75	Ile	Phe	Ile	Phe	80 GTA		
65					70					13					00		
gct 1	ttt	ata	caa	ata	ccc	act	tta	atg	act	atc	ata	atc	tct	tat	act	2	89
Ala	Phe	Ile	Gln	Ile	Pro	Thr	Leu	Met	Thr	Ile	Ile	Ile	Ser	Tyr	Thr		
				85					90					95			
cgt (ata	ctc	ttt	gat	att	ctg	aaa	aaa	aag	tct	gaa	aag	ggc	aga	agc	3	337
Arg '	Val	Leu	Phe	Asp	Ile	Leu	Lys	Lys	Lys	Ser	Glu	Lys	Gly	Arg	Ser		
			100					105					110				4,
aaa	acc	ttc	tcc	aca	tac	aac	acc	cat	cta	ctt	tct	gtc	tca	ttg	tac	3	385
Lys .	Ala	Phe	Ser	Thr	Cys	Gly	Ala	His	Leu	Leu	Ser	Val	Ser	Leu	Tyr		
-		115					120					125					
						2+~	tat	ata	cat	cct	aca	tct	aac	tta	gct		433
Tac Tar	gga	act Thr	Len	Ile	Phe	Met	Tvr	Val	Arg	Pro	Ala	Ser	Gly	Leu	Ala		
_	130	****	204			135					140						
														- 4- 4-			401
gaa	gac	caa	gac	aaa	gtg	tat	tct	ctg	Phe	Tur	acg Th∽	att Ile	ata Ile	Ile	ccc Pro	•	481
145	ASP	GIII	asp	пўs	150		OCT.	eu		155					160		
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ctg																	487
Leu	Leu																

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Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala 130 135 140

Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro 145 150 155 160

Leu Leu

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ctc Leu	tgt Cys	gtc Val	ttc Phe 20	tta Leu	gtg Val	gct Ala	gta Val	tct Ser 25	cgg Arg	att Ile	ctg Leu	tct Ser	tgt Cys 30	gcc Ala	agc Ser	97
		tct Ser 35														145
		gtc Val														193
		tca Ser														241
		gtc Val														289
		.Glà														337
		ttg Leu 115														385
		tca Ser														433
		aag Lys									Thr					481

atg ttg
Met Leu
487

<210> 227

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<212> PRT

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<223> Taxon = 9606; gene = HSA10; Accession DDBJ/EMBL/GenBank = AF179760

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Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His . 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Asp Thr Pro 145 150 150 160

Met Leu

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			(487	•												
			ict =	olf	acto	ry r	ecep	tor								
	> 2															40
															c atg	49
	1 A.	a Il	.e Cy		e Pr	о Ге	u Hi	s T			а 11	e Me	et Se		o Met	
1				5					10	1				15)	
			gcc	~+~	~+~	~~~	ata	taa	+~~	~+~	a+a	200	200	++-	cat	97
			Ala													,
neu	cys	neu	20	neu	vaı	AIG	пеа	25	пр	var	пец	1111	30	rne	1113	
			20					23					50			
acc	ato	tta	cac	act	tta	ctc	atα	acc	agg	tta	tat	ttt	tat	αca	σac	145
			His													
ALU	2100	35		****	J-04	204	40		5			45			2	
		-														
aat	ata	atc	ccc	cac	ttt	ttc	tat	gat	atg	tct	gct	ctg	ctg	aag	ctg	193
			Pro													
	50					55	_	-			60					
gcc	ttc	tct	gac	act	cga	gtt	aat	gaa	tgg	gtg	ata	ttt	atc	atg	gga	241
Ala	Phe	Ser	Asp	Thr	Arg	Val	Asn	Glu	Trp	Val	Ile	Phe	Ile	Met	Gly	
65					70					75					80	
			ctt													289
Gly	Leu	Ile	Leu	Val	Ile	Pro	Phe	Leu	Leu	Ile	Leu	Gly	Ser		Ala	
				85					90					95		
			tcc													337
Arg	Ile	Val	Ser	Ser	Ile	Leu	Lys		Pro	Ser	Ser	Lys		Ile	Cys	
			100					105					110			
																205
			tct													385
Lys	Ala		Ser	Thr	Cys	GIA		His	Leu	Ser	Val		Ser	Leu	Pne	
		115					120					125				
													•		L _L	422
			gtt						_			-		-		433
Tyr		Thr	Val	ITe	GŢĀ		Tyr	Leu	Cys	Ser		Ala	Asn	ser	ser	
	130					135					140					

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135

130

Met Leu

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tac Tyr	ata Ile	gtc Val	aga Arg 100	aca Thr	att Ile	ctg Leu	aag Lys	ttc Phe 105	cct Pro	tct Ser	gtt Val	cag Gln	caa Gln 110	agg Arg	aaa Lys	337
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gtg Val 145	gcc Ala	ata Ile	aat Asn	aaa Lys	gga Gly 150	gtt Val	tca Ser	gtt Val	ctt Leu	act Thr 155	act Thr	tct Ser	gtc Val	gca Ala	ccc Pro 160	481
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90 95

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75

70

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aaa Lys	gca Ala	ttg Leu 115	tcc Ser	aca Thr	tgt Cys	ggc Gly	tcc Ser 120	cat His	ctc Leu	tct Ser	gtg Val	gtg Val 125	tct Ser	ctc Leu	tat Tyr	385	
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Sei	: Leu	Ser 35	His	: Thr	Leu	Leu	Leu 40	ı Thr	Arg	, Leu	. Ser	Phe 45	: Суз	: Ala	Ala		
Ası	n Thi 50	c Ile	e Pro) His	. Val	. Phe 55	e Cys	a As <u>r</u>) Let	a Ala	Ala 60	a Lev	ı Lev	ı Lys	; Leu		
Se:	r Cy:	s Se:	r Ası	o Ile	Phe 70	e Lev	ı Ası	ı Glı	ı Let	ı Val 75	L Met	: Phe	· • Thi	· Val	l Gly 80		

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

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Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 115 120 125

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478

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Leu	суз	Thr	Leu 20	Leu	Val	Leu	Сув	Ala 25	Trp	Leu	Ser	Gly	Phe 30	Leu	Thr		

Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser 35 40 45

Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu 55

Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala 70

Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met 85

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys · 100 105

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 120

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Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro 150 155

Met Leu

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97

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gca ttq atq cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag 145

WO 01/46262									247	7					PC 1/L	D00/0201/
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atg Met																485
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Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln

Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu 50 55 60

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly 65 70 75 80

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val 85 90 95

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe 115 120 125 :

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<220>

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tgc tgc ctg a Cys Cys Leu M	atg ctg gtg Met Leu Val 20	Ala Ala	tcc tgg c Ser Trp L 25	tc tgc tcc eu Cys Ser	cac tgc His Cys 30	ctg Leu	97
gct ttc tct c Ala Phe Ser I 35	etc acc ctt Leu Thr Leu	ctg atg Leu Met 40	act cag t Thr Gln F	tc tca ttc he Ser Phe 45	tgt gcc Cys Ala	tcc Ser	145
cat tcc atc of His Ser Ile of 50	caa cac ttt Gln His Phe	ttc tgt Phe Cys 55	gat gta c Asp Val E	cc cca ctc Pro Pro Leu 60	ctc aaa Leu Lys	ctt Leu	193
gcc tgt tca g Ala Cys Ser A 65	gac acc cat Asp Thr His 70	atc ttt Ile Phe	Gln Val 7	aca atg tta Thr Met Leu 75	act gaa Thr Glu	gga Gly	241
gtc ctc tca (Val Leu Ser (ggt gtg atc Gly Val Ile 85	cct ctt Pro Leu	acc tgt of Thr Cys V	gtc ctg gtc Val Leu Val	tct tat Ser Tyr 95	gcc Ala	289
cac atc atg	cac acc atc His Thr Ile 100	ctc agg	atc cct d Ile Pro S 105	cct gct ggg Ser Ala Gly	ggc aag Gly Lys 110	cac His	337
aaa gtc ttc Lys Val Phe	tct acc tgt Ser Thr Cys	ggc tct Gly Ser	cac ctg	tca gtg gtc Ser Val Val	act ctc Thr Leu	ttc Phe	385

115 120 125

tat ggg acc ctc ttt ctg gtg tat ttc cag cct tca tcc tcc tac tca

Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser

130 135 140

gca gat act gga atg gtg gca tgt gta gta tac acg atg gtc acc ccc 481
Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
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atg gtg
Met Val

<210> 246

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Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu 20 25 30

Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser 35 40 45

His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu 50 55 60

Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly 65 70 75 80

Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala 85 90 95

His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His . 100 105 110

Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe

115 120 . 125

Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser 130 135 140

Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro 145 150 150 160

Met Val

<223	> 6 > 1 > 1 > 1 > 1 > 1 > 1 > 1 > 1 > 1 > 1	nisc_ (1) Taxor CDS (2)	nur f feat (487 1 = 1	ure () .3515	; ge				Acc	cessi	on I)DBJ/	'EMBI	J/Ger	ıBank =	AF179774
<400		247												. .		40
										al Al					n Thr	49
gtc	tgc	aga	aga	ctt	gtc	ttt	tgt	tgt	tgg	gta	gct	ggt	ctg	ttt	att	97
			Arg 20													
ata	atc	cct	cca	ctt	agc	ctg	ggc	cta	aat	ctg	gaa	ttt	tgt	gat	tct	145
			Pro													
gat.	acc	att	gat	cat	ttt	atc	tat	σat	gca	tct	ccc	ctc	cta	aat	atc	193
			Asp													
tct	tat	tca	aat	act	tgg	ttc	atg	gaa	cag	act	gtt	atc	atc	tgt	gca	241
			Asn													
ata	ctg	acc	ctc	att	atg	aca	ctt	atg	tgt	gta	gtt	ctg	tcc	tac	att	289
_	_		Leu													
			aag									-				337
Tyr	Ile	Ile	Lys	Thr	Ile	Leu	Gly	Phe	Ser	Ser	Ala	Gln	Gln	Lys	Lys	

WO 01/46262	2		252		PCT/IB00/02017
•	100	105		110	•
aaa gcc ttt i Lys Ala Phe i 115	tcc acc tgt (Ser Thr Cys (tct tcc cac Ser Ser His 120	atg att gtg Met Ile Val	gtg tcc atc Val Ser Ile 125	acc 385 Thr
tat ggc agc Tyr Gly Ser 130	Tyr Ile Phe	atc tat atc Ile Tyr Ile 135	aaa cct tct Lys Pro Ser 140	gca aag gaa Ala Lys Glu	gaa 433 Glu
gta gcc att Val Ala Ile 145	aac aag ggt Asn Lys Gly 150	gtg aca gtc Val Thr Val	ctc act act Leu Thr Thr 155	tcc atc gcc Ser Ile Ala	CCC 481 Pro 160
atg ctg Met Leu					. 487
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Ile Ile Pro 35	Pro Leu Ser	Leu Gly Leu 40	ı Asn Leu Glu	Phe Cys Asp 45	Ser
Asp Thr Ile 50	Asp His Phe	Ile Cys Ası 55	o Ala Ser Pro 60	Leu Leu Asn	Ile
Ser Cys Ser 65	Asn Thr Trp 70	Phe Met Gl	u Gln Thr Val 75	. Ile Ile Cys	Ala 80
			•		

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile 85 90 90 95

100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr 1.15 120 125 $\cdot\cdot\cdot$

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu 130 135 140

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro 145 150 150 160

Met Leu

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WO 01/46262		254		PCT/IB00/02017		
85		90	95			
cac atc gtg aga acg His Ile Val Arg Thr 100	Ile Leu Arg I	att cct tct act a le Pro Ser Thr 8	agt cag agg a Ser Gln Arg '	aca 337 Thr		
aag gcc ttt tct aca Lys Ala Phe Ser Thr 115	tgt tct tcc c Cys Ser Ser E 120	His Met Ile Val	atc tcc atc Ile Ser Ile 125	tct 385 Ser		
tat ggc agc tgc att Tyr Gly Ser Cys Ile 130	ttt atg tac a Phe Met Tyr 1 135	att aag ccc tca [le Lys Pro Ser . 140	gca aag gat Ala Lys Asp	aga 433 Arg		
gta tct ttg agc aag Val Ser Leu Ser Lys 145	gca gtg gct g Ala Val Ala V 150	gtg cta atc acc Val Leu Ile Thr 155	tca gta gct Ser Val Ala	ccc 481 Pro 160		
atg ctc Met Leu				487		
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Val Cys Thr Leu Let 20	ı Val Phe Ala	Ser Trp Leu Val 25	Ser Phe Leu 30	Ile .		
Val Phe Pro Ala Le 35	ı Met Leu Leu 40	Leu Lys Leu Asp	Tyr Cys Gly 45	Phe		
Asn Ile Ile Asp Hi 50	s Phe Thr Cys 55	Asp Tyr Phe Pro 60	Leu Leu Gln	Leu		
Ser Cys Ser Asp Th	r Lys Phe Leu 70	Glu Ile Met Gly 75	Phe Ser Cys	Ala 80		

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met

85 90 95

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg 130 135 140

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro 145 150 155 160

Met Leu

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<211> 487

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1	u Al	a 11	e cy	5 5		0 20	.u	<u>.</u>	10					15	•		
ctg Leu	gct Ala	aca Thr	cag Gln 20	ctg Leu	gcc Ala	ttg Leu	Gly	tcc Ser 25	tgg Trp	gtc Val	tgt Cys	ggt Gly	ttc Phe 30	ctg Leu	gcc Ala	97	,
att Ile	gca Ala	gtg Val 35	ctg Leu	acg Thr	gcc Ala	ctt Leu	atc Ile 40	agt Ser	ggc Gly	ctg Leu	tcc Ser	ttc Phe 45	tgt Cys	ggc Gly	gcc Ala	145	i
cgt Arg	gcc Ala 50	atc Ile	aac Asn	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	att Ile	gca Ala	ccc Pro 60	tgg Trp	att Ile	gcc Ala	ctg Leu	193	J
gcc Ala 65	tgc Cys	acc Thr	agc Ser	aca Thr	cag Gln 70	gca Ala	ata Ile	gag Glu	ctc Leu	gtg Val 75	gcc Ala	ttt Phe	gtg Val	att Ile	gct Ala 80	241	L
ttt Phe	gtg Val	gtc Val	atc Ile	ctg Leu 85	agt Ser	tca Ser	tgc Cys	ctc Leu	atc Ile 90	acc Thr	ctg Leu	gtc Val	tcc Ser	tac Tyr 95	gtg Val	289	•
tac Tyr	att Ile	atc Ile	agc Ser 100	acc Thr	atc Ile	ctc Leu	agg Arg	atc Ile 105	cca Pro	tct Ser	gcc Ala	agc Ser	ggc Gly 110	cgg Arg	agc Ser	33′	7
aaa Lys	gcc Ala	ttc Phe 115	tct Ser	acg Thr	tgc Cys	tcc Ser	tct Ser 120	His	ctc Leu	acc Thr	gtg Val	gtg Val 125	ctc Leu	atc Ile	tgg Trp	38	5
tat Tyr	ggg Gly 130	Ser	acg Thr	att Ile	ttt Phe	ctt Leu 135	His	gtc Val	cgc Arg	acc Thr	tcc Ser 140	Ile	aca Thr	gac Asp	gcc Ala	43	3
ttg Leu 145	Asp	ctg Leu	acc Thr	aaa Lys	gct Ala 150	. Val	cat His	gtc Val	ctg Leu	aac Asn 155	Thr	gtg Val	gtg Val	act Thr	cca Pro 160	48	1
	cta Leu															48	7

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Val Leu

145

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geo ego aca oog ood geo eer ger eer egs eeg ge	97
Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile	
20 25 30	
ged eco cod god oco dog eco con any con god on con	.45
Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe	
35 40 45	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.93
and all all gas the tree are type gas the tree are the	.93
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu 50 60	
50 55 60	
tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct	41
Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala	
65 70 75 80	
gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg	89
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met	
85	
cac acc ges ass are res as as as as	337
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr	
100 105 110	
and acc acc acc acc acc acc acc acc acc ac	385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser	
115 120 125	
	122
cat ggo ago ogo act tot and the act and the second	133
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg	
130 135 140	
gta tot ttg ago aag goa gtg got gtg ota ato aco toa gta got coo	481
Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro	
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Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro

150

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Me	t Al	la Il	le Cy	s Hi	s Pr	o Le	u Ai	g Ty	r Pi	o Va	ıl Ph	e Me	et As	n Hi	s Arg	
1				5					10)				15	5	
gtg	tgt	ctc	ttc	ctg	gca	tct	ggc	tgc	tgg	ttc	ctg	gga	tca	gta	gat	97
Val	Cys	Leu		Leu	Ala	Ser	Gly		<u> L</u> LD	Phe	Leu	Gly		Val	Asp	•
			20					25					30			
																4.5
				act												145
Gly	Phe		Leu	Thr	Pro	Ile		Met	Thr	Phe	Pro		Cys	Arg	Ser	
		35					40					45				
																102
cgg	gag	att	cac	cat	tcc	ttc	tgc	gaa	gtc	CCL	gct	gta	acg	acg	CCC	193
Arg		Ile	His	His	Ser		Cys	GLu	Val	Pro		vaı	Thr	Thr	ren	
	50					55					60					
											- t-	+	a+ a	+~~	tat	241
				acc												241
	Cys	ser	Asp	Thr		Leu	туг	GIU	Met		Mer	TAL	nea	Cys	80	
65					70					75					80	
							~+~	303	a+a	a++	tas	= ~~	tac	tat	tca	289
				ctc Leu												203
vaı	ьeu	Mec	ьeu		TIE	Pro	val	TILL	90	TIE	Ser	Ser	per	95	Ser	
				85					90					,,		
	a++	ata	ata	acc	2+4	G2G	200	ato	aac	tca	aca	aaa	aac	caa	aad	337
				Thr												337
Pile	TIE	neu		TIII	116	III	A. y	105	CLY	DCL	ALU	Olu	110	9	232	
			100					100					110			
			~~~	acc	+~+	too	taa	Cac	ato	200	ata	att	atc	ctc	ttc	385
				Thr												303
цĀS	ALA	115	мта	TIIL	Cys	Ser	120		nec	1111	var	125	110			
		*13					3.20					-4J				
+-+	~~~	~~~	~~~	atc	tec	acc	tac	ata	ctc	ccc	acc	tee	tac	Cac	act	433
				Ile												
TÄT			uld	TTG	- X -	135	+3+	11CC	Teu		140	061	-7-			
	130					133					T-40					

cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct 481 Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 155 150 488 gtg cta a Val Leu <210> 257 <211> 162 <212> PRT <213> Eulemur fulvus <220> <221> misc_feature <222> (1)..(488) <223> Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779 <400> 257 Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp 25 20 Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser 40 Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu 55 Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys 65 Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser 85 Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys 105 100 Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe 125 115 120

Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr

135

Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro 155 150 145

Val Leu

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<212> DNA

<213> Eulemur fulvus

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tgtgctgacc ctgaatatga ctctaacttg tgtagttctg tcatacgctt acatcatcaa 300

gacaattttt agattccctt ctgtccagca aaggaaaaag gccttttcca cctgttcttc 360

ccacatgatt gtggtttcca tcacctatgg cacgtgcatt ttcatctaca tgaatcctac 420

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gacccgtgtg gctttctgtg cccagaaggc catcccccac ttctactgtg atcccagtgc 180

tctcctgaag ctcgcctgct cggatacccg cataaatgag ctgatgatca tcgccatggg 240

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ggctgtgctt ggcatctcgt ctcctggcgg gcgatgcaag gccttctcca cctgtggttc 360

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ctc tgc acc tta ttg gtg gct ata tcc tgg ctc ctg tct tgt gcc agc Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser 20 25 30	97
tcc ctc tcc cac acc ctt ctc ctg acc cgg ctg tcc ttc tgt gct gct Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala 35 40 45	145
aat gtc att ccc aac ttc ttc tgt gac ctt gct gct ctg ctc aag ctg Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60	193
tcc tgc tca gac atc ttc ctc aat gag ctg gtc atg ttt aca gta ggg Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80	241
gtg gtg gtc att acc ttg cca ttc tta tgt atc ctg gta tct tac ggc Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95	289

337 tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc tgc Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys 105 aaa gca tta tcc acg tgt ggg tcc cat ctc tct gtg gtg tct ctg tac 385 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 120 433 tac ggg gca ata ttt ggg cag tac ctt ttc cca gca tta agc aat tcc Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser 130 135 481 att gac aag gac atc att gtg gct atg atg tac acg gtg gtc aca ccc Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro 155 150 145 487 atg ttg Met Leu

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Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys 105 100 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr 120 Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser 135 Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro 155 150 145 Met Leu <210> 264 <211> 475 <212> DNA <213> Eulemur rubriventer <220> <221> misc_feature <222> (1)..(475) <223> Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785 <220> <221> CDS <222> (2)..(475) <223> Product = olfactory receptor <400> 264 c gtg gca atc tgc aag cct ctt cat tac atg aat att atg agt cgt caa 49 Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln 10 ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac 97 Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His 25 20 tct att att cag att ttt atc acc atc caa tcg ccc ttt tgt ggt ccc 145 Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro 40 35 aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt 193 Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu 55 50 gcc tgc acc gac acc ttt gta gag ggg ctg act gtg ttg gcc aat agt 241 Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser 75 70

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att Ile	att Ile	ctg Leu	gtg Val 100	cac His	ttg Leu	agg Arg	aaa Lys	cat His 105	tct Ser	gca Ala	gag Glu	GJA aaa	agg Arg 110	cac His	aaa Lys	337
gcc Ala	ctc Leu	tct Ser 115	acc Thr	tgt Cys	gcc Ala	tct Ser	cac His 120	atc Ile	acg Thr	gtg Val	gtc Val	att Ile 125	ttg Leu	ttt Phe	ttt Phe	385
gga Gly	cct Pro 130	gcc Ala	atc Ile	ttc Phe	ctc Leu	tac Tyr 135	atg Met	cga Arg	cct Pro	tcc Ser	tct Ser 140	acc Thr	ttc Phe	aca Thr	gaa Glu	433
gac Asp 145	aaa Lys	ctc Leu	atg Met	ggt Gly	gtg Val 150	ttg Leu	tac Tyr	aca Thr	gtc Val	atc Ile 155	acc Thr	ccc Pro	agt Ser			475
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	Leu Val 100	His Le	eu Arg		His 9 105	Ser i	Ala (	Glu (		Arg 1 110	His I	Lys	
Ala Leu	Ser Thr 115	Cys A.	la Ser	His 120	Ile '	Thr '	Val '		Ile : 125	Leu :	Phe	Phe	
Gly Pro 130	Ala Ile	Phe L	eu Tyr 135		Arg	Pro		Ser 140	Thr	Phe '	Thr	Glu	
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Leu Cys	Ile Cys	Phe I	lle Ilo	e Cys	Ser 25 ttc	Tyr	Thr	Gly gat	Gly ttt	Phe 30 tgt	Val ggt	Asn	97 145
Leu Cys gca ata Ala Ile	Ile Cys 20 ata tta Ile Leu	Phe I acc a Thr S	le Ilo agc aa Ser As	e Cys c aca n Thr 40 c tgt	Ser 25 ttc Phe	Tyr acg Thr	Thr ttg Leu	gat Asp	ttt Phe 45	Phe 30 tgt Cys	yal ggt Gly aag	Asn gac Asp ttg	
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								252	<b>+</b> 6 6	200	222	aac	cac	ctc	337
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75

70

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aaa gcc ttt tcc Lys Ala Phe Ser 115	act tgt tcc to Thr Cys Ser Se 12	er His Ile Ile	gtt gtt tcc ct Val Val Ser Le 125	c tct 385 u Ser
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gtg act tta agc Val Thr Leu Ser 145	aaa gga gta go Lys Gly Val Al 150	et gtg gtt aat la Val Val Asn 155	Thr Ser Val Al	t cct 481 a Pro 160
ctt ttg Leu Leu				487
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Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg 130 135 140

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Leu Leu

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<210> 273

<211> 486

<212> DNA

<213> Eulemur rubriventer

<220>

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g tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat eu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp 20 25 30	97
c ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac a Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp 35 40 45	145
t gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc u Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50 55 60	193
g tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct a Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala 70 75 80	241
gc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act vs Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr 85 90 95	289
aa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat In Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100 105 110	337
na gcc ttt tcc acc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc ys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385
at ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct yr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 130 135 140	433
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<211> 161

<212> PRT

<213> Eulemur rubriventer

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<400> 274

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Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp 35 40 45

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu 50 55 60

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala 65 70 75 80

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr 85 90 95

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser 130 135 140

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Cys

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1				5					10	l				10		
		ggt	aka	ata	~++	+ ==	ctt	tcc	cta	tcc	att	tac	tcc	aca	gat	97
ctg	Cyc	Gly	cty Len	Len	yıı Val	Ser	Len	Ser	Leu	Ser	Ile	Cvs	Ser	Ala	Asp	
neu	cys	Gry	20	шеш	144			25				•	30		_	
gcc	ctg	ctc	cac	agc	ctc	atg	ctg	ctg	cag	ctg	tcc	ttc	tgc	aca	gac	145
Ala	Leu	Leu	His	Ser	Leu	Met	Leu	Leu	Gln	Leu	Ser	Phe	Cys	Thr	Asp	
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													~+ ~		ata	193
ctt	gaa	atc	tcc	ctt	ttc	ttc	tgt	gaa	gtc	gtt	Cla	gtc	gcc val	Tare	Len	193
Leu		Ile	ser	ьeu	Pne	55	Cys	GIU	Val	· val	60	VAI	Val	БуЗ	шец	
	50					33					•					
aca	tac	tcc	gat	acc	ctc	atc	aac	aac	ctt	ctg	atc	tat	ttt	gca	gct	241
Ala	Cys	Ser	Asp	Thr	Leu	Val	Asn	Asn	Leu	Leu	Ile	Tyr	Phe	Ala	Ala	
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tgc	acc	ttg	ggt	ggc	att	cct	ctg	tct	ggc	atc	att	ttt	tct	tac	act	289
Cys	Thr	Leu	Gly		IIe	Pro	Leu	ser	90	TIE	TTE	Pne	Ser	95	TIIT	
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caa	ata	gcc	acc	tcc	att	tta	aaa	ato	cca	tca	tca	ggc	aga	aag	tat	337
Gln	Ile	Ala	Thr	Ser	Ile	Leu	Lys	Met	Pro	Ser	Ser	Gly	Arg	Lys	Tyr	
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Lys	Ala	Phe	Ser	Ala	Cys	Gly		His	Leu	Ser	Val	Val	Ser	Leu	Phe	
		115					120					125				
A A.		aca	~~+	++~	~~~	ata.	tac	atc	ant	tct	aca	att	tet	gac	tct	433
m-	999	Thr	Glv	Leu	G1 v	Val	Tur	Tle	Ser	Ser	Ala	Val	Ser	Asp	Ser	
TAT	130		Gry	Dea	0.2.3	135	-1-		502		140			~		
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Ser	Arg	Arg	Thr	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	
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Val	Leu															

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Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro

155

150

Val Leu

<210>	277														
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	Maca	a sy	Ivani	us											
<220>	-i	foot													
	misc														
	(1).	. (#00 ^	1 516.	~~~		MCV1	72.	Acce	ssin	ח חח	B.T/E	MBL/	GenB	ank =	AF179792
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Pro Al	n Tle	Cyc	Cln	Pro	Len	Ara	Tvr	Ara	Val	Leu	Met	Asn	His	Arg	
	a iie	Cys	5	110			-1-	10					15	_	
1			,												
ctc tg	t ata	cta	cta	ata	gga	act	acc	taa	atc	ctc	tgc	ctc	ctc	aag	96 .
Leu Cy	re Val	Len	Leu	Val	Glv	Ala	Ala	Trp	Val	Leu	Cys	Leu	Leu	Lys	
nen cy	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	20					25	_				30			
		- •													
tcg gt	g act	σασ	aca	gtc	att	gcc	atg	agg	ctg	ccc	ttc	tgt	ggc	cac	144
Ser Va	al Thr	Glu	Thr	Val	Ile	Ala	Met	Arg	Leu	Pro	Phe	Cys	Gly	His	
	35					40					45				
cac gt	tg gto	agt	cac	ttc	acc	tgc	gag	atc	ctg	gcg	gtg	ctg	aag	ctg	192
His Va	al Val	Ser	His	Phe	Thr	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	
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acg to	gc ggt	aac	aca	tcg	gtc	agc	gag	gtc	ttc	ctg	ctg	gtg	ggc	tcc	240
Thr C	ys Gly	Asn	Thr	Ser	Val	Ser	Glu	Val		Leu	Leu	Val	GIĀ	Ser	
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													<b>.</b>		288
atc c	tg ct	, ctg	cct	gtg	ccc	ctg	gca	ttc	att	tgc	ctg	TCC	Tac	Lug	200
Ile L	eu Lei	ı Leu		Val	Pro	Leu	Ala		TIE	Cys	ьeu	Ser	95	пеп	
			85					90					95		
										~at	~at	~~~	tac	cac	336
ctc a	tc ct	ggc	acc	atc	ctg	agg	gtg	Dec	Cox	315	ycc λla	999 Glv	Cve	Ara	330
Leu I	le Le			TTE	Leu	Arg			Ser	ALG	AIG	110	Cys	ni g	
		100					105								
	cc tt	_ 4		+	+ 0 2	~~~	C20	cta	act	ata	ata	ata	ctt	ttc	384
aaa g	la Ph	e tee	mb-	cyc	Com	31a	ui.	Lou	Δla	val	Wal	Len	Len	Phe	
ras v			TILL	Cys	Ser	120		Бец			125				
	11	<b>ɔ</b>				120									
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rac a	igc ac Ser Th	∪ αιC ~ τ1-	TIA	Dhe	acy mh≠	Ture.	Mot	Lve	Pro	Lvs	Ser	Lvs	Glu	Ala	•
_		T TT6		FILE	135			. <u> </u>		140					
7	L30					•									
000	atc to	+ ~=+		r ata	tto	: aca	artic	etc	: tac	: acc	: ato	gto	aca	ccc	480
uie T	lle Se	r Acr	. gli	, goo	Phe	Thr	Va!	Le	TVI	Ala	Met	. Val	Thr	Pro	
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147															

PCT/IB00/02017 WO 01/46262

atg ttg Met Leu 486

<210> 278

<211> 162

<212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792

<400> 278

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His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu 50 55

Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser 75 70 65

Ile Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu 90 85

Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg 110 105

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe 115

Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala 135 130

His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro 150 155 145

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                                                                    120
aacgtttatg teettttgtg gagacaacet tgteaateae tacatgtgtg accteettee
                                                                    180
tctccttgag ctctcttgca acagcactta cataaatttg ctggtggttt ttattattgt
                                                                     240
gaccaatggc attggggtgc caattgtcac catttttatc tcttatggtt ttattctttc
                                                                     300
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cacataattg tggtatcgct gttctttggg tcaggtgctt tcatgtacct cacaccacct
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 <223> product = olfactory receptor
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  Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
                                      10
                                                                      97
 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat
 Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
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gga Gly	ggg ggg	atc Ile 35	cag Gln	act Thr	ttg Leu	ttc Phe	ata Ile 40	gcc Ala	cac His	tta Leu	cca Pro	ttc Phe 45	tgt Cys	ggc Gly	cct Pro	145
aat Asn	gtc Val 50	atc Ile	gac Asp	cac His	ttt Phe	atg Met 55	tgt Cys	gat Asp	tta Leu	gta Val	cct Pro 60	ctt Leu	cta Leu	gag Glu	ctg Leu	193
gcc Ala 65	tgc Cys	aca Thr	gac Asp	act Thr	cac His 70	acc Thr	ttg Leu	Gly	cct Pro	ctg Leu 75	ata Ile	gct Ala	gcc Ala	aac Asn	agt Ser 80	241
gga Gly	tca Ser	ttg Leu	tgt Cys	ttc Phe 85	ctc Leu	att Ile	ttt Phe	tcc Ser	atg Met 90	ctg Leu	gtt Val	gct Ala	tcc Ser	tat Tyr 95	gtc Val	289
atc	atc Ile	ctg Leu	tgc Cys 100	Ser	cta Leu	agg Arg	act Thr	cat His 105	Ile	tct Ser	gaa Glu	ggg	cgt Arg 110	cac His	aaa Lys	337
gtt Val	ctg Leu	tct Ser 115	Ser	tgt Cys	acc Thr	tct Ser	cat His 120	Ile	ttt Phe	gtt Val	gtc Val	atc Ile 125	tta Leu	ttc Phe	ttt Phe	385
Val	Pro 130	Cys	Ser	Tyr	ctg Leu	Tyr 135	Leu	Arg	Pro	Leu	Thr 140	Ser	Phe	Phe	Pro	433
act Thr 145	Asp	aaa Lys	gct Ala	gtg Val	act Thr 150	Val	ttt Phe	tgc Cys	acc Thr	Leu 155	Phe	aca Thr	cct Pro	atg Met	ttg Leu 160	481
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Me	t Cy	s Gl	y Pho 20	e Le	u Me	t Gl	y Va	1 Al 25		y Ile	e Le	u Gly	y Phe 30	e Val	l His	

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro 35

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu 50 55 60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser 65 70 75 80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val 85 90 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
100 105 110

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe 115 120 125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro 130 135 140

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu 145 150 155 160

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<211> 402

<212> DNA

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<222> (1)..(402)

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<400> 282

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ctaaatcttg acttctgtgc ctgcctccaa cgtcattaat catttctact gtgacactac 180
tccactcctg cagatttcct gcactgacac acagctcctg gacaggatgg gattcatttc 240
agcattggtg acactcttag tcacattggt aatggtgatg gtatcatgat atccctttct 300
tatggcagtt gcatcttcat gtatgttaag ccatcggtca aacaaaagat atattttca 360
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<221>	CDS (407)															
<222>	• • • •															
	23> Product = olfactory receptor															
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_	Ala	a II	е Су		n Pr	о ге	и ье	и ту			u va	ı va	ı se	15	o Lys	
1				5					10					1.0		
gta t					~+~	+	ata	202	+=0	ctt	cac	aat	ctt	atc	aca	97
Val C	gt d	egt	CLG	Lou	ycy Wal	Cor	T.OU	Whr	Tur	Len	Cay	Ser	T ₁ e11	Tle	Thr	٠.
val C	ys A	arg	20	пеп	Val	SET	пеп	25	+ <b>y</b> +	200	<b></b>	DC_	30			
			20					23					-			
gcc c	tt :	act	atc	tet	tee	t.at.	ata	ttc	tct	ata	tca	tac	tat	tct	tcc	145
Ala L	en '	Thr	Val	Ser	Ser	Cvs	Val	Phe	Ser	Val	Ser	Tvr	Cys	Ser	Ser	
		35				-4-	40					45	_			
		-														
aac a	tc a	atc	aac	cat	ttt	tac	tgt	gac	gat	gtc	cct	ttg	cta	gca	ttg	193
Asn I	le :	Ile	Asn	His	Phe	Tyr	Cys	Asp	Asp	Val	Pro	Leu	Leu	Ala	Leu	
5						55	_				60					
tcg t	gt	tct	gat	acc	tac	att	cca	gaa	aca	gca	gtg	ttt	atc	ttt	tca	241
Ser C	ys	Ser	Asp	Thr	Tyr	Ile	Pro	Glu	Thr	Ala	Val	Phe	Ile	Phe	Ser	
65					70					75					80	
ggg a	CC	aat	ttg	ttt	ttc	tcc	atg	acc	gtt	gtt	ctg	ata	tcc	tac	ttc	289
Gly T	hr	Asn	Leu	Phe	Phe	Ser	Met	Thr		Val	Leu	Ile	Ser		Phe	
				85					90					95		
																227
aac a	itt	gtt	att	acc	att	ttg	agg	ata	cgt	tcc	tca	gaa	gga	cga	caa	337
Asn I	le	Val		Thr	Ile	Leu	Arg		Arg	ser	ser	GIU		Arg	GIN	
			100					105					110			
					hh.			~~~		2+2	~a+	a+a	~++	~+~	ttc	385
aaa g Lys A																303
rys A	та		Ser	Thr	cys	Ald	120	UTS	Met	TTG	Ала	125	Val	Val	THE	
		115					120					123				
tat g		- ~ t-	at-	a++	++~	at~	tat	++~	Caa	CCS	add	act	aat	cac	tca	433
Tyr G																
		THE	пец	nen	FIIE	135	TÄT	neu	GTI	110	140	551	******			
	130					133					_ = 0					
tta g	ra+	act	gac	222	atσ	gee	tea	atc	ttc	tac	acc	cta	atc	ata	cct	481
Leu A																
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atg ttg Met Leu 487

<210> 284

<211> 162

<212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796

<400> 284

Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys

5 · 10

Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr 20 25 30

Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser 35 40 45

Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu 50 55 60

Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser 65 70 75 80

Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe 85 90 95

Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Phe 115 120 125

Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser 130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro 145 150 155 160

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gct ci Ala Le	tt tt eu Le 35	eu H	ac i	act Thr	ctc Leu	ctc _. Leu	ctg Leu 40	gcc Ala	tgg Trp	ctt Leu	tcc Ser	ttc Phe 45	tgt Cys	gct Ala	gat Asp	145
cac at	le I	tc c le P	ro :	cac His	ttc Phe	ttc Phe 55	tgt Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ttg Leu	193
tcc to Ser Co	gc to ys Se	ca g er A	sp (ac	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80	241
ttg a Leu T	ca go	cc a la I	itt [le	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgt Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly	289
cac a His T	ict g hr A	la V	gtc /al 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	Pro	tct Ser	act Thr	aat Asn	ggc Gly 110	ata Ile	tgc Cys	337
aaa g Lys A	Ala L	tg t eu s .15	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	His	ctc Leu	tca Ser	gca Ala	gtg Val 125	act Thr	ctc Leu	tat Tyr	385
tat g Tyr G	ggg a Sly T 130	cc a	att Ile	att Ile	ggt Gly	ctc Leu 135	Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	Ser	agc Ser	aac Asn	act Thr	433

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W O 01/40202	287	

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

atg ttg
Met Leu

<210> 286

<211> 162

<212> PRT

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(487).

<223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797

<400> 286

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Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr 115 120 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 55 560

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<221	> C	CDS															
<222	> (																
<223																	
<400> 287																	
t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met																	
1 5 10 15																	
														++-	as t	97	
ctc	tgt	ctc	gcc	ctg	gtg	gcg	ctg	tcc	tgg -	gta	ctg	acc	acc mb	Dho	uac uic	31	
Leu	Cys	Leu	Ala	Leu	Val	Ala	Leu		Trp	vaı	ьeu	Thr	TILL	Pile	UTP		
			20					25					30				
														~~~	<b>~</b> 2.0	145	
gcc	atg	tta	cac	act	tta	ctc	atg	gcc	agg	ttg -	tgt	בננ	cgt.	31a	yac Nan	. 143	
Ala	Met		His	Thr	Leu	Leu		Ala	Arg	Leu	Cys	Pne	Cys	Ala	ASD		
		35					40					45					
																102	
aat	gtg	atc	ccc	cac	ttt	ttc	tgt	gat	atg	tct	gct	ctg	ctg	aag	ctg	193	
Asn	Val	Ile	Pro	His	Phe	Phe	Cys	Asp	Met	Ser		Leu	Leu	Lys	Leu		
	50					55					60						
			•														
gcc	tgc	tct	gac	act	caa	gtt	aat	gaa	ttg	gcg	ata	ttt	atc	acg	gga	241	
Āla	Cys	Ser	Asp	Thr	Gln	Val	Asn	Glu	Leu	Ala	Ile	Phe	Ile	Thr	Gly		
65	-		-		70					75					80		
aaa	cta	att	ctt	atc	atc	cca	ttc	cta	ctc	atc	ctt	ggg	tcc	tat	gca	289	
Glv	Len	Tle	Leu	Val	Ile	Pro	Phe	Leu	Leu	Ile	Leu	Gly	Ser	Tyr	Ala		
GIJ				85					90					95		•	
				••													
	-++	ata	tcc	tcc	atc	ctc	aac	atc	cct	tca	tct	aag	ggt	atc	tgc	337	•
3	TIA	1757	Ser	Cor	Tle	Len	Lvs	Val	Pro	Ser	Ser	Lvs	Gly	Ile	Cys		
Arg	116	val			110	204	_, _	105				_	110		-		
			100					103									
		L. L	tet		+	~~~	+	C=C	ctc	tat	ata	ata	tca	ata	ttc	385	5
aag	gcc	כככ	tet	act	Cyc	Clar	200	uic	Len	Car	ycy Val	Wal	Ser	Len	Phe		
Lys	Ala		Ser	Thr	Cys	GIĀ			neu	per	val	125	Der	204			
		115	1				120					145					
							.			~~~	+	~~+	22+	art-	tet	433	3
tat	ggg	acc	gtt	att	. ggt	CEC	Lac	LLC	Lgc	. cca	. cca	yet	aat	ugt			-

289

Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser 130 135 140

act cta aag gag act gtc atg gct atg atg tac act gtg gtg acc ccc

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro

145

150

160

atg ctg 487 Met Leu

<210> 288

<211> 162

<212> PRT

<213> Macaca sylvanus

<220>

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<222> (1)..(487)

<223> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

<400> 288

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
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Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60

Ala Cys Ser Asp Thr Gln Val Asn Glu Leu Ala Ile Phe Ile Thr Gly 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser

130 135 140

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro 145 150 155 160

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<213>	- M	Macaca sylvanus														
<220>	•															
<221>	misc_feature															
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	223> Product = olfactory receptor															
<400> 289																
a tgt gcc atc tgc tgc ccc ctc cac tac acc aca gcc atg agc cct aag Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys																
_	s Al	a Il	е Су		s Pr	o Le	u Hi	s Ty			r Al	a me	t Se			
1				5					10	l				15)	
						-			-	~+ a		+a+	~+ ~	ata	tat	97
ctc t	tgt	atc	tta	CEC	CLL	Coo	ttg	Core	m _m	y.c	Lua	202	y Ly tra l	Lou	There	31
ren (.ys	тте	ьеu 20	Leu	nea	261	Бец	25	тъ	val	Deu	PET	30	Deu	- X -	
			20			•		23					30			
ggc (a+ a	2+2	a=a	200	++0	ctc	ata	acc	aca	ata	acc	ttc	tat	aaa	tca	145
Gly I																
GTA 1	ueu	35	urs	1111	LIIC	пси	40					45	0,0	 2		
		55														
cga a	aaa	atc	cac	tac	atc	ttc	tat	σασ	atq	tat	qta	tta	ctg	agg	ctg	193
Arg 1																
	50			- 4		55	-			_	60			_		
	_															
gca	tgt	tcc	gac	act	cag	att	aat	cac	aca	gtg	ctg	att	gcc	aca	ggc	241
Ala	Cys	Ser	Asp	Thr	Gln	Ile	Asn	His	Thr	Val	Leu	Ile	Ala	Thr	Gly	
65	_				70					75					80	
tgc																289
Cys	Phe	Ile	Phe	Leu	Ile	Pro	Phe	Gly	Phe	Met	Ile	Ile	Ser	\mathtt{Tyr}	Val	
				85					90					95		
ttg																337
Leu	Ile	Val	Arg	Ala	Ile	Leu	Arg	Ile	Pro	Ser	Val	Ser	Lys	Lys	Tyr	
			100					105				•	110			
aaa																385
Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Gly	Val	Val	Ser	Leu	Phe	

WO 01/46262	291		PCT/IB00/02017
115	120	125	4
tat ggg aca ctt tgt atg gta Tyr Gly Thr Leu Cys Met Val 130 135	Tyr Leu Lys Pro Leu	His Thr Tyr Se	t 433 c
gtg aag gac tca gta gcc aca Val Lys Asp Ser Val Ala Thr 145	gtg atg tat gcg gtg Val Met Tyr Ala Val 155	gtg aca ccc atg Val Thr Pro Mer 16	t
atg Met			484
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<213> Macaca sylvanus			
<220>			
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	MSY179; Accession D	יסטי EMBL/GenBan	V - WLTISISS
<400> 290 Cys Ala Ile Cys Cys Pro Leu	ı His Tvr Thr Thr Ala	Met Ser Pro Lv	s
Cys Ala Tie Cys Cys Pio Heo	1 1113 1y1 1111 1111 1111		

Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr 20 25 30

10

Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser 35 40 45

Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu 50 55 60

Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly 65 70 75 80

Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val 85 90 95

Leu Ile Val Arg Ala Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr
100 105 110 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Gly Val Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Cys Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser 130 135 140

Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met 145 5 5 150

Met

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gacccagctg totttotgtg ctgcgaacac catcccccac atcttotgtg accttgctgc
cctgctcaag ctgtcctggt cagatatctt cctcaatgag ctggtcatgt tcacagtagg
                                                                    240
ggtggtggtc attaccctgc cattcatgtg tatcctggta tcatatggct acactggggc
                                                                   300
caccatcctg agggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc
ccatctctct gtggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac
                                                                    420
tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc
                                                                    480
                                                                    487
cgtgttg
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<210> 292
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<211> 487

<212> DNA

<213> Macaca sylvanus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9546; gene = MSY181; pseudogene; Accession DDBJ/EMBL/GenBank = AF179801

<400> 292

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cttagtggct gtatcttgaa tt	ctgtcttg tgcca	gctcc ctctctcaca	cccttctcct	120
gacccagctg tctttctgtg ct	gcgaacac catcc	cccac atcttctgtg	accttgctgc	180
cctgctcaag ctgtcctggt ca	gatatete ectea	atgag ctggtcatgt	tcacagtagg	240
ggtggtggtc attaccctgc ca	ttcatgtg tatcc	tggta tcatatggct	acactggggc	300
caccatectg agggtecett ca	accaaagg gatco	acaaa gcattgtcca	catgtgcctc	360
ccatctctct gtggtttctc to	tattatgg gtcaa	tattt ggccagtaac	atttcccaac	420
tgtaagcagt tctattgaca ag	gatgttac tgtgg	ctctc atgtacatcg	tggtcacacc	480
cgtgttg				487
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gtg tgt acc tta tta gtc Val Cys Thr Leu Leu Val 20	ctc tgc agt tg Leu Cys Ser Tr 25	gg gtg gct ggc tt p Val Ala Gly Le 30	eu Met Ile	97
att gtt cca cca ctg agc Ile Val Pro Pro Leu Ser 35	tta ggc ctc ca Leu Gly Leu G 40	ag ctc gaa ttc to In Leu Glu Phe Cy 45	gt ggc tcc ys Gly Ser	145
aat gcc att gat cat ttt Asn Ala Ile Asp His Phe 50	agc tgt gat go Ser Cys Asp A 55	ca ggt cct ctc ct la Gly Pro Leu Le 60	ca aag atc eu Lys Ile	193
tca tgc tca gac aca tgg Ser Cys Ser Asp Thr Trp 65. 70	gta ata gaa c Val Ile Glu G	ag ata gtt ata co ln Ile Val Ile Lo 75	tt atg gct eu Met Ala 80	241
gta ttt gca ctc att atc Val Phe Ala Leu Ile Ile	acc cta gtt t Thr Leu Val C	gt gtg att ctg to ys Val Ile Leu So	cc tac ttg er Tyr Leu	289

WO 01/46262		294	PCT/IB00/02017
	85	90	95
tac ata gtc aga Tyr Ile Val Arg 100	aca att ctg agg tt Thr Ile Leu Arg Ph 10	cc cct tct gtt cag caa ne Pro Ser Val Gln Gln .	agg aaa 337 Arg Lys
aag gcc ttt tct Lys Ala Phe Ser	acc tgt tca tcc ca Thr Cys Ser Ser Hi	ac atg att gtg gtt tcc is Met Ile Val Val Ser	att gcc 385 Ile Ala

tat gga agc tgc atc ttc gtc tat atc aag ccc tct gca aaa gat gaa

Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu

130 135 140

120

gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtt gca ccc
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
145 150 155 160

ttg ttg Leu Leu

<210> 294

<211> 162

<212> PRT

<213> Macaca sylvanus

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115

<223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802

<400> 294

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Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser 35 40 45

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile 50 55 60

Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala 65 70 75 80

Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu 85 90 95

Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys 105 110 100 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala 120 Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu 135 130 Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro 150 155 Leu Leu <210> 295 <211> 487 <212> DNA <213> Callithrix jacchus <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803 <220> <221> CDS <222> (2)..(487) <223> Product = olfactory receptor <400> 295 . . . t gtg gcc att tgc cgc ccc ctg tac tac tcc aca gtc atg agc ccc caa 49 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln 1 gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt 97 Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val 25 145 gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr 35 ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta 193 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu 55 50 241 tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly

75

70

									23	.0							
ggc Gly	aca Thr	gta Val	ctc Leu	att Ile 85	gtc Val	ccc Pro	ttt Phe	ata Ile	tgc Cys 90	att Ile	gtc Val	acc Thr	tcc Ser	tac Tyr 95	atc Ile		289
cac His	att Ile	gtg Val	cct Pro 100	gct Ala	atc Ile	ctg Leu	agg Arg	gtc Val 105	cga Arg	acc Thr	tgt Cys	ggt Gly	ggg Gly 110	gcg Ala	ggc Gly		337
aag Lys	gcc Ala	ttt Phe 115	tcc Ser	acc Thr	tgc Cys	agt Ser	tcc Ser 120	cac His	ctc Leu	tgc Cys	att	gtt Val 125	tgt Cys	ata Ile	ttc Phe		385
tat Tyr	ggg Gly 130	acc Thr	ctc Leu	ttc Phe	agt Ser	gcc Ala 135	tac Tyr	ctg Leu	tgt Cys	cct Pro	ccc Pro 140	Ser	att Ile	gcc Ala	tct Ser		433
gaa Glu 145	Glu	aag Lys	gac Asp	att Ile	gca Ala 150	gca Ala	gct Ala	gca Ala	ctg Leu	tat Tyr 155	Thr	ata Ile	gtg Val	act Thr	ccc Pro 160		481
_	ttg Leu																487
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Ala	a Lei	a Th: 35	r Hi:	s Th	r Lei	ı Let	Met 40	t Ala	a Ar	g Le	u Se:	r Pho	e Cy:	s Val	l Thr		
Gl	y Gl 50	u Il	e Al	a Hi	s Pho	e Pho 55	e Cy	s As	p Il	e Th	r Pr 60		l Le	u Ly:	s Leu		
Se 65	_	s Se	r As	p Th	r Hi 70	s Il	e As	n Gl	u Me	t Me 75		l Ph	e Va	l Le	u Gly 80		

Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile 90 85 His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly 105 100 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe 120 115 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 130 Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro 155 150 145 Met Leu <210> 297 <211> 486 <212> DNA <213> Callithrix jacchus <220> <221> misc_feature <222> (1)..(486) <223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/GenBank = AF179804 <220> <221> CDS <222> (1)..(486) <223> Product = olfactory receptor <400> 297 gtg gcc atc tgt cac cca ctg cac tac aca gtc acc att aac ccc aga 48 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg 5 ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 96 Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 tee tea tta caa ace tta ata gtg etg egg ett tee tte tge aca gae 144 Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 40 ttg gaa atc ccc cgc ttt ttc tgc gaa ctt aat cag gtc atc cac ctt 192

Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu

V	VO 01	l/4626	52						29	8					PCT/IB	00/02017
gcc Ala 65	tgt Cys	tct Ser	gac Asp	act Thr	ttt Phe 70	ctt Leu	aat Asn	gat Asp	gtg Val	gtg Val 75	atg Met	tat Tyr	ttg Leu	gcc Ala	gct Ala 80	240
gtg Val	ctg Leu	ctg Leu	GJÀ āāā	ggt Gly 85	ggt Gly	ccc Pro	ctt Leu	gca Ala	90 GJA aaa	att Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr 95	tct Ser	288
aag Lys	ata Ile	gtt Val	tcc Ser 100	tcc Ser	ata Ile	cgt Arg	gca Ala	atc Ile 105	tca Ser	tca Ser	gct Ala	cag Gln	ggg Gly 110	aag Lys	tac Tyr	336
aag Lys	gca Ala	ttt Phe 115	tcc Ser	acc Thr	tgt Cys	gta Val	tct Ser 120	cac His	atc Ile	tta Leu	att Ile	gtc Val 125	tcc Ser	tta Leu	ttt Phe	384
tat Tyr	ggt Gly 130	aca Thr	ctc Leu	cta Leu	ggt Gly	gtg Val 135	tac Tyr	ctt Leu	agt Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn	432
tca Ser 145	cat His	tca Ser	aga Arg	gct Ala	gca Ala 150	gcc Ala	tcg Ser	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160	480
_	ctg Leu															486

<210> 298
<211> 162
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/ GenBank = AF179804
<400> 298
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1 5 10 15

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45

Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 50 55 60

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 299 <211> 487 <212> DNA <213> Callithrix jacchus <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805 <220> <221> CDS <222> (2)..(487) <223> Product = olfactory receptor <400> 299 c gtg gcc atc tgt aac cca ctg ttg tac atg gtc acc atg tct ccc cag Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln 97 gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gct ttg ggg Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly 20 gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt gca gaa 145

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu 35 40 45

acc ctt gtc aat cac tac atg tgt gac atc ctt ccc ctc ctt gag ctc

Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 50 55 60

tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val

70

75

80

acc att ggc att ggg gtg ccc att gtc acc att ttt atc tct tat ggt

Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly

85 90 95

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser

100 105 110

aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc 385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Leu Leu Phe
115 120 125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro

130 135 140

ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
145 150 155 160

atg ttt 487
Met Phe

<210> 300

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805

<400> 300

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1 5 10 15

Val Cys Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly 20 25 30

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu 35 40 45

Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu

50. 55 60

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80

Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe 115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 150 160

Met Phe

<210> 301

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA196; Accession DDBJ/EMBL/GenBank = AF179806

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 301

c ttg gcc atc tgc cac ccg ctg cac tac tcc tcc aag atg agc ctg tgc
Leu Ala Ile Cys His Pro Leu His Tyr Ser Ser Lys Met Ser Leu Cys
1 10 15

97

agc tgc acc cta atg ttg ggc tgc tta tgg acc act gcc agc ctc cat

Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His
20 25 30

gcc ctt ctg cac acc ctt ctc ttg gcc cgg ctg gac ttc tgt gcc agc
Ala Leu Leu His Thr Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser

WO 01/46262		302	PCT/IB00/02017
35	40	45	
aat gtt atc ccc tac t Asn Val Ile Pro Tyr P 50			_
tcc tgt tct gac acc c Ser Cys Ser Asp Thr A 65	-		
ggc ctg atc atc ctc c Gly Leu Ile Ile Leu L 85	-		
tgc att gca gct gca g Cys Ile Ala Ala Ala V 100		l Pro Ser Ala Arg	·
aag gcc ttt tcc acc t Lys Ala Phe Ser Thr C 115			
tat ggc acc atc tca g Tyr Gly Thr Ile Ser G 130			
aca gac aag gac tca c Thr Asp Lys Asp Ser L 145			
atg ctg Met Leu			487
<210> 302 <211'> 162 <212> PRT <213> Callithrix jac <220> <221> misc_feature <222> (1)(487) <223> Taxon = 9483; <400> 302 Leu Ala Ile Cys His F	gene = CJA196		IMBL/GenBank = AF179806 Ser Leu Cys
1 5		10	15
Ser Cys Thr Leu Met I 20	seu Giy Cys Le 25	u TIP THI THE ALA	30
Ala Leu Leu His Thr I	Leu Leu Al	a Arg Leu Asp Phe	Cys Ala Ser

Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu 50 55 60

Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly 65 70 80

Gly Leu Ile Ile Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr 85 90 95

Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe 115 120 125

Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser His Ser 130 135 140

Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro 145 150 155 160

Met Leu

<210> 303

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 303

t gtt gcc ata tgt cac cca ctg cac tac aca gtc acc att aac ccc aga

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg

1 5 10 15

97

ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30

tcc Ser	tca Ser	tta Leu 35	caa Gln	acc Thr	tta Leu	ata Ile	gtg Val 40	ctg Leu	cgg Arg	ctt Leu	tcc Ser	ttc Phe 45	tgc Cys	aca Thr	gac Asp		145
ttg Leu	gaa Glu 50	atc Ile	ccc Pro	cac His	ttt Phe	ttc Phe 55	tgc Cys	gaa Glu	ctt Leu	aat Asn	cag Gln 60	gtc Val	atc Ile	cac His	ctt Leu		193
				act Thr													241
gtg Val	ctg Leu	ctg Leu	Gly ggg	ggt Gly 85	ggt Gly	ccc Pro	ctt Leu	gca Ala	aga aga	att Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr 95	tct Ser		289
				tcc Ser													337
			Ser	acc Thr													385
tat Tyr	ggt Gly 130	aca Thr	ctc Leu	cta Leu	ggt Gly	gtg Val 135	tac Tyr	ctt Leu	agt Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn		433
tca Ser 145	cat His	tca Ser	aga Arg	gct Ala	gca Ala 150	gcc Ala	tcg Ser	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160		481
_	ctg Leu																487
<21 <21 <21		304 162 PRT															
<21 <22		Call	ithr.	ix j	acch	us											
<22	1>		_	ture	:												
<22		Taxo	.(48 on =		; ge	ne =	: CJA	197;	Acc	essi	on D	DBJ/	EMBL	/Gen	Bank	= AF	179807
Val 1	Ala	ılle	e Cys	His 5	Pro	Leu	His	: Тут	Thr 10	Val	. Thr	: Ile	Asn	Pro 15	Arg		

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 50 55 60

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 305

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 305

c att gcc atc tgt agc ccc ttg ctg tac aat gtc atc atg tcc tat cac

Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His

1 5 10 15

ttc Phe	tgc Cys	ttc Phe	cgg Arg 20	ctc Leu	aca Thr	gtg Val	gga Gly	gtt Val 25	tac Tyr	att Ile	tta Leu	ggc	atc Ile 30	ctt Leu	gga Gly		97
tct Ser	aca Thr	att Ile 35	cac His	acc Thr	agc Ser	tct Ser	atg Met 40	ttg Leu	aga Arg	ctc Leu	ttt Phe	ctg Leu 45	tgc Cys	aaa Lys	act Thr		145
aat Asn	gtg Val 50	att Ile	aac Asn	cat His	tat Tyr	ttt Phe 55	tgt Cys	gat Asp	ctc Leu	ttc Phe	cct Pro 60	ctc Leu	ttg Leu	gaa Glu	ctc Leu		193
tcc Ser 65	tgc Cys	tcc Ser	agt Ser	acc Thr	tac Tyr 70	atc Ile	aat Asn	gaa Glu	tta Leu	cta Leu 75	gtt Val	ctg Leu	gtc Val	ttg Leu	agt Ser 80		241
gca Ala	ttg Leu	aat Asn	atc Ile	ctg Leu 85	acg Thr	cct Pro	gcc Ala	tta Leu	act Thr 90	atc Ile	ctg Leu	gcc Ala	tct Ser	tat Tyr 95	atc Ile		289
ttc Phe	acc Thr	att Ile	gcc Ala 100	agt Ser	atc Ile	ctc Leu	cac His	att Ile 105	cgc Arg	tcc Ser	act Thr	gag Glu	ggc Gly 110	agg Arg	tcc Ser	,	337
aaa Lys	gcc Ala	ttc Phe 115	agc Ser	act Thr	tgc Cys	agc Ser	tcc Ser 120	cac His	atc Ile	tca Ser	gct Ala	gtt Val 125	gct Ala	gtc Val	ttc Phe		385
ttt Phe	gga Gly 130	Ser	gca Ala	gca Ala	ttc Phe	atg Met 135	Tyr	ctg Leu	cag Gln	cca Pro	tca Ser 140	Ser	gtc Val	agt Ser	tcc Ser		433
atg Met 145	Asp	cag Gln	Gly	aaa Lys	gtg Val 150	Ser	tct Ser	gtg Val	ttt Phe	tac Tyr 155	Thr	act Thr	gtt Val	gtg Val	ecc Pro 160		481
_	ctg Leu																487
<21 <21		306 162															
<21		PRT Call	ithr		acch	1119							•				
<22	0>																
		misc (1).			•												
<22	3>	Taxo	n =	9483	; ge	ene =	CJA	198;	Acc	essi	on I	DBJ/	EMBI	J/Ger	Bank	= A	F179808
	0> • Ala	306 11e	e Cvs	: Sei	Pro	Let	ı Lev	ı Tyı	. Asr	ı Val	. Ile	e Met	: Sei	: Туз	His		
1				5					10					15			

Phe Cys Phe Arg Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly 20 25 30

Ser Thr Ile His Thr Ser Ser Met Leu Arg Leu Phe Leu Cys Lys Thr 35 40 45

Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu 50 60

Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser 65 70 75 80

Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile 85 90 95

Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe 115 120 125

Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser 130 135 140

Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro 145 150 155 160

Met Leu

<210> 307

<211> 469

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(469)

<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809

<220>

<221> CDS

<222> (2)..(469)

<223> Product = olfactory receptor

<400> 307

WO 01/46262		308	PCT/IB00/02017
t gtt gct atc tg Val Ala Ile Cy 1	rt cac ccc ctg cars His Pro Leu Hi	c tac acc act gtc a s Tyr Thr Thr Val I	atg agt cgg gga 49 Met Ser Arg Gly 15
tta tgc tgt gtg Leu Cys Cys Val 20	ttg gtt gct gcc Leu Val Ala Ala	tcc tgg atg gga gg: Ser Trp Met Gly Gl: 25	a ttt gtg cac 97 y Phe Val His 30
tcc acc gtc cag Ser Thr Val Gln 35	acc att ctc act Thr Ile Leu Thr 40	atc cgt ctg ccc tt Ile Arg Leu Pro Ph 45	t tgt ggg cca 145 e Cys Gly Pro
aat cag gtg gac Asn Gln Val Asp 50	aac ttt ttt tgt Asn Phe Phe Cys 55	gat gtt ccc cct gt Asp Val Pro Pro Va 60	c atc aaa ctt 193 l Ile Lys Leu
gcc tgt gct gac Ala Cys Ala Asp 65	act ttt gtc att Thr Phe Val Ile 70	gaa ttg ctc atg gt Glu Leu Leu Met Va 75	a tct aac agt 241 l Ser Asn Ser 80
ggg ttg atc tcc Gly Leu Ile Ser	acc agc tcc ttt Thr Ser Ser Phe 85	gtg gtg ctg att to Val Val Leu Ile Se 90	c tcc tac acc 289 r Ser Tyr Thr 95
act atc cta gtc Thr Ile Leu Val 100	Lys Ile His Ser	aag gag gga agg cg Lys Glu Gly Arg Ar 105	ra aag gca ctc 337 rg Lys Ala Leu 110
tcc aca tgt gcc Ser Thr Cys Ala 115	tct cac ctt atg Ser His Leu Met 120	gtg gta aca ctt tt Val Val Thr Leu Ph 12	e Gly Pro Cys
agt ttc atc tat Ser Phe Ile Tyr 130	cct cat cct ttc Pro His Pro Phe 135	tct aca ttt tct gt Ser Thr Phe Ser Va 140	g gac aag atg 433 al Asp Lys Met
gtg tct gta ctc Val Ser Val Lev 145	tac aag gtt att Tyr Lys Val Ile 150	act cca atg cta Thr Pro Met Leu 155	. 469
<210> 308 <211> 156 <212> PRT			

<210> 308
<211> 156
<212> PRT
<213> Callithrix jacchus
<220>
<221> misc_feature
<222> (1)..(469)
<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809
<400> 308
Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly
1 5 10 15

Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His 20 25 30

Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro

Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu 50 55 60

Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met Val Ser Asn Ser 65 70 75 80

Gly Leu Ile Ser Thr Ser Ser Phe Val Val Leu Ile Ser Ser Tyr Thr 85 90 95

Thr Ile Leu Val Lys Ile His Ser Lys Glu Gly Arg Arg Lys Ala Leu 100 105 110

Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Gly Pro Cys 115 120 125

Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met 130 135 140

Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu 145 150 155

<210> 309

<211> 488

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 309

c gtt gcc att tgc ttc ccc ctt cgc tat atg cta ctc atg agc cat tcc

Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser

1 5 10 15

97

att tgt gtc acg atg att ata gtt tgt tgg tcc att agc ata gct ggg

Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 25 20

gcc ctg atc ctc act gtc ttc acc atg cat ctg cct tat tgt ggc ccc 145 Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro 45 35

tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg 193 Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 50

gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc atc ttg ggt 241 Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 75

ttc atc ctg ctt ttg gtc cca ctc tcc ctc atc ctg gcc tct tac gtc 289 Phe Ile Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val 85

ttc atc ttt gcc tct atc ttc aga atc cgc tca gcg cag ggg agg ctc 337 Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu 100 105

aag too tto too acg tgt get too cac gto act gtg gto acc atg tto 385 Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 120

tat ggg ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac 433 Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135

cca gag cgg gac aag aag cta gcg ctg ttc tac aat gtg gtc tct ggc 481 Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly 155 150 145

488 ttc ctc a Phe Leu

<210> 310

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

<400> 310

Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser 5

Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20 25 30

Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro 35 40 45

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 50 55 60

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 65 70 75 80

Phe Ile Leu Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val 85 90 95

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu 100 105 110

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 115 120 125

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135 140

Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly 145 150 150

Phe Leu

<210> 311

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 311

t gtg gca att tgc cac ccc tta cgt tac act gcc aca atg aac ctg cgc 49

Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ala Thr Met Asn Leu Arg

1 10 15

ctt tgt gtc cag cta gtg gct gga ctg tgg ctt gtt act tac ctc cat

97
Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
20 25 30

gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc 145

gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc 145
Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
35 40 45

aat atc atc cat cat ttc ttc tgt gat ctc aac cct cta cta cgg ctc

Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu

50 55 60

tct tgc tct gcc gtc tcc ttc aac gta atg atc att ttt gca gta gga
Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
70 75 80

ggt cta ttg gct ctc acg ccc ctt gtc tgt atc ctc gta ttt tat gga 289
Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
85 90 95

ctt atc ttc tcc act gtt ctg aag atc acc tct act cag ggg aaa cag
Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
100 105 110

aga gct gct tcc acc tgc ggc tgc cac ctg tca gta gtg gtg ctg ttt

Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Leu Phe

115 120 125

tat ggc aca gcc att gcc gtc tac ttt agc ccc tca tcc tcc cat acg
Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser His Thr
130 135 140

481

cct gag agt gac act ctc tcg acc gtc atg tat tca gtg gtg gcc ccg
Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
145 150 155 160

atg ctg . 487 Met Leu

<210> 312

<211> 162

<212> PRT

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811

<400> 312

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WO 01/46262 313

1 5 10

Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His 20 25 30

Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe 35 40 40

Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu 50 55 60

Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly 65 70 80

Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly 85 90 95

Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
100 105 110

Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Val Leu Phe 115 120 125

Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Ser His Thr 130 135 140

Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro 145 150 155 160

Met Leu

<210> 313

<211> 491

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(491)

<223> Taxon = 9600; gene = PPY110; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179812

<400> 313

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                                                                     120
aatgtttatg teettttgtg gagacaacet tgtcaateae tatetgtgtg acateettee
                                                                     180
tctccttgag ctctcctgca acagctctta cataaatttg ctggtggttt ttattattgt
                                                                     240
gaccattggc attggggtgc caattgtcac catttttatc tcttatggtt ttattctttc
                                                                     300
cagcattete cacattaget cacagaggge aggteaggte taaagcette agtacetgea
                                                                     360
gttcccacat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac
                                                                     420
                                                                     480
caccttetet tetacecetg gaccagggga aagtgteete catttttat aetgetgtgg
                                                                     491
tgcccatgtt t
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<210> 314
<211> 480
<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(480)
<223> Taxon = 9600; gene = PPY111; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179813
<400> 314
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                                                                    120
tggccaggtt gtgtttttgt gcagacaatg tgatccccca ctttttctgt gatatgtctg
                                                                    180
ctctgctgaa gctgtcctgc tctgacactc gagttaatga attggtgata tttatcatgg
                                                                     240
gagggeteat tettgteate ceatteetae teateettgg gteetatgea egaattgtet
                                                                     300
cctccatcct caaggtccct tctaagggta tctgcaaggc cttctctact tgtggctccc
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acctctctgt ggtgtccctg ttctatggga ccgttagtgg tctctactta tgcccatcgg
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<210> 315
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480

ctaatagttc tactctgaag gagactgtca tggctgtaat gtacactgtg gtgaccccca

<211> 486

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814

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cag tgt gtc Gln Cys Val	atg ctg Met Leu 20	gtg gct Val Ala	ggg to Gly Se 25	r Trp	gtc a	atc q Ile i	Ala	tgt Cys 30	gcg Ala	tgt Cys	96
gct ctt ttg Ala Leu Leu 35	His Thr	Leu Leu	Leu Al 40	a Arg	Leu	Ser	Phe 45	Cys	Ala	Asp	144
cac atc atc His Ile Ile 50	tct cac Ser His	ttc ttc Phe Phe 55	tgt ga Cys As	c ctt p Leu	Gly .	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	192
tcc tgc tca Ser Cys Ser 65	Asp Thr	Ser Leu 70	Asn Gl	n Leu	Ala 75	Ile	Phe	Thr	Ala	80 GlA	240
ttg aca gcc Leu Thr Ala	Ile Met 85	Leu Pro	Phe Le	eu Cys 90	Ile	Leu	Val	Ser	Тут 95	Gly	288
cac att ggg His Ile Gly	Val Thr	: Ile Leu	Gln II	le Pro)5	Ser	Thr	Lys	Gly 110	Ile	Cys	336
aaa gcc ttg Lys Ala Leu 115	Ser Thi	c Cys Gly	120	is Leu	Ser	Val	Val 125	Thr	Ile	Tyr	384
tat ggg aca Tyr Gly Thi 130	r Ile Ile	e Gly Leu 135	Tyr P	he Leu	. Pro	Pro 140	Ser	Ser	Asn	Thr	432
aat gac aag Asn Asp Lys 145	g aac ata s Asn Ile	a att gct e Ile Ala 150	tca g a Ser V	tg ata al Ile	tac Tyr 155	aca Thr	gta Val	gtc Val	act Thr	Pro 160	480
atg ttg Met Leu								•			486

<210> 316

<211> 162

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814

<400> 316

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Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 · 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

Met Leu

<210> 317

<211> 487

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature <222> (1)..(487) <223> Taxon = 9600; gene = PPY113; pseudogene; Accession DDBJ/EMBL/GenBank = AF179815 <400> 317 cactgccatt tgccaccctc taagataaac caatctcatg agacccaaaa tttgtggact 60 tatgactgcc ttctcctgga tcctgggctc tacggatgga atcattgatg ctgcagcgac 120 attttccttc tcctactgtg ggtctcggga aatagcccac ttcttctgtg agttcccttc 180 catactaatc ctctcatgca atgacacatc aatatttgaa aaggttcttt tcatctgctg tatagtaatg attgtttttc ctgttgcaat catcatcgct tcctatgctc aagttattct 300 ggctgtcatt cacatgggat ctggagaggg tcgtcggata gctttcacga cctgttcctc 360 tcacctcatg gtggtgggaa tgtactatgg agcagctttg ttcatgtaca tacggcccac 420 atctgatcgc tcccctacac aggacaagat ggtgtctgta ttctacacca tcctcactcc 480 487 catgctg <210> 318 <211> 484 <212> DNA <213> Pongo pygmaeus <220> <221> misc_feature <222> (1)..(484) <223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816 <220> <221> CDS <222> (2)..(484) <223> product = olfactory receptor <400> 318 t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 1 ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97 Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25 20 gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 40 35 193 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu

50

•	VO 01	1/4626	52						31	.8			,		PCT/IB00/02017		
tcc Ser 65	tgc Cys	tct Ser	gac Asp	act Thr	cga Arg 70	gtt Val	aat Asn	gaa Glu	ttg Leu	gtg Val 75	ata Ile	ttt Phe	atc Ile	atg Met	gga Gly 80	241	
GJA aaa	ctc Leu	att Ile	ctt Leu	gtc Val 85	atc Ile	cca Pro	ttc Phe	cta Leu	ctc Leu 90	atc Ile	ctt Leu	Gly ggg	tcc Ser	tat Tyr 95	gca Ala	289	

cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag 337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
100 105 110

gcc ttc tct act tgt ggc tcc cac ctc tct gtg gtg tcc ctg ttc tat

Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr

115

120

125

ggg acc gtt agt ggt ctc tac tta tgc cca tcg gct aat agt tct act
Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
130 135 140

ctg aag gag act gtc atg gct gta atg tac act gtg gtg acc ccc atg
Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met
145 150 155 160

ctg Leu

<210> 319

<211> 161

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

<400> 319

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met 1 5 10 15

Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
100 105 110

Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr 115 120 125

Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr 130 135 140

Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Val Thr Pro Met 145 5 50 150

Leu

<210> 320 <211> 483 <212> DNA <213> Pongo pygmaeus <220> <221> misc_feature <222> (1)..(483) <223> Taxon = 9600; gene = PPY115; Accession DDBJ/EMBL/GenBank = AF179817 <220> <221> CDS <222> (1)..(483) <223> Product = olfactory receptor <400> 320 48 gtg gcc gtc tgc cac cca ctg cat tac acg ctc atc atg cat gga ggg Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly 5 96 Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn 20 tcc ctg atg gaa aca att atc acc ttc cag ctt ctc ctg tgt cac aat 144 Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Cys His Asn 45 35 40

gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc

PCT/IB00/02017 WO 01/46262 320 Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 55 tgt gtg gac gtc tcc ttc aac aag gcc atg gtg gcc atc tca ggg ttt 240 Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe 70 ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac 288 Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 85 ata gtt gct gcc att ctt cat att cct tct gcc cag gga cgc cgc aaa 336 Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys 105 gcc ttt ggg act tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt 384 Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 120 115 ggg gct aca atg ttc acc tac atg aga cct gcg ggc ggc tcc tcc ctg 432 Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 135 gaa aag aag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg 480 Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 155 150 145 483 ctt Leu <210> 321 <211> 161 <212> PRT <213> Pongo pygmaeus <220> <221> misc_feature <222> (1)..(483) <223> Taxon = 9600; gene = PPY115; Accession DDBJ/EMBL/GenBank = AF179817 Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly

Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn 20 25 25 30

10

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Cys His Asn 35 40 45

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala

50 55 60

Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe 65 70 75 80

Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 85 90 95

Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys
100 105 110

Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 115 120 125

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 130 135 140

Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 145 150 155 160

Leu

<210> 322

<211> 484

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(484)

<223> Taxon = 9600; gene = PPY116; Accession DDBJ/EMBL/GenBank = AF179818

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 322

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Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1 5 10 15

tcc ctg atg gaa aca att atc acc ttc cag ctt ccc ctg tgt cac aat

145
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn

,	VO 0:	1/4626	52				322								PC	T/IB00/02017
		35					40					45				
gtt Val	att Ile 50	aat Asn	cac His	ttt Phe	gcc Ala	tgt Cys 55	gag Glu	acc Thr	tta Leu	gca Ala	gtg Val 60	cta Leu	cga Arg	cta Leu	gcc Ala	193
			gtc Val													241
			ctg Leu													289 -
	_		gcc Ala 100													337
			acc Thr													385
			atg Met													433
	Lys		aat Asn													481
ctt Leu																484
<22	1> 2> 3> 0>		о ру													
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<40	0>	323													Gly	

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn

Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn

25

323

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala 55 Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe 70

Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His 90

Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys

Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe 120

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu 135 140 130

Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met 155 150 145

Leu

<210> 324 <211> 479 <212> DNA <213> Pongo pygmaeus <220> <221> misc_feature <222> (1)..(479) <223> Taxon = 9600; gene = PPY117; pseudogene; Accession DDBJ/EMBL/GenBank = AF179819 <400> 324 60 tgtagccata tgcaaaccct tatactatgt ggtcatcatg agccgaagga cacgcactgt cttggtaatg atctcctggg ctgtgggctt ggtgcacaca ttaagccagt tatcatttac 120 tgtgaacctg ccttttttgt ggacctaatg tagtagacag ctttttttgt gatcttcctc 180 gagtgaccaa acttgcctgc ctggactctt acctcattga aatactaatt gtggtcaata 240 gtggagttct ttccctaagc actttctgtc tcttggtcag ctcctacatc attattcttg 300

ttatggtttg gctcaagtct tcggctgcaa tggcgaaggc attttctacg ctggcttccc 360
atattgcagt agtaatatta ttctttggac cttgcatctt catctatgtg tggcccttta 420
ccatctatcc tttggataaa cttcttgcca tattttacac tgttttcacc cccatccta 479

<210	> 3	25											•			
<211	> 4	487 .														
<212	> D	DNA														
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<220>																
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<222> (2)(487)																
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Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser																
	1 5 10 15															
cao	tat	atc	atg	cta	ata	gct	ggg	tcc	tgg	gtc	atc	gct	tgt	gcg	tgt	97
Gln	Cys	Val	Met	Leu	Val	Ala	Gly	Ser	\mathtt{Trp}	Val	Ile	Ala	Cys	Ala	Cys	
	-		20					25					30			
gct	ctt	ttg	cat	acc	ctc	ctt	ctg	gcc	cgg	ctt	tcc	ttc	tgt	gct	gac	145
Ala	Leu	Leu	His	Thr	Leu	Leu	Leu	Ala	Arg	Leu	Ser		Cys	Ala	Asp	
		35					40					45				
																102
cac	atc	atc	tct	cac	ttc	ttc	tgt	gac	CTT	ggt	gcc	ctg	CTC	aag	ccg	193
His		IIe	Ser	His	Pne		Cys	Asp	теп	GIY	60	ьец	ьeu	цуs	пеа	
	50					55					00					
		*	gac	200	tcc	ctc	aa+	CaG	tta	пса	atc	+++	aca	gca	gga	241
Cor	Cve	Cor	Asp	Thr	Ser	Len	Asn	Gln	Leu	Ala	Ile	Phe	Thr	Ala	Glv	
65	Cys	Der	nsp		70					75					80	
Ų,					. •											
tta	aca	acc	att	atg	ctt	cca	ttc	ctg	tgc	atc	ctg	gtt	tct	tat	ggt	289
Leu	Thr	Ala	Ile	Met	Leu	Pro	Phe	Leu	Cys	Ile	Leu	Val	Ser	Tyr	Gly	
				85					90					95		
cac	att	ggg	gtc	acc	atc	ctc	cag	att	CCC	tcc	acc	aag	ggc	ata	tgc	337
His	Ile	Gly	Val	Thr	Ile	Leu	Gln	Ile	Pro	Ser	Thr	Lys		Ile	Cys	
			100					105					110			
																205
aaa	gcc	ttg	tcc	act	tgt	gga	tcc	cac	ctc	tca	gtg	gtg	act	atc	tat	385
Lys	Ala		Ser	Thr	Cys	Gly			Leu	Ser	Val			TTE	туr	
		115					120					125				
L - J			- L- L-		~	a.c	+-+	+++	a++		000	+	240	220	acc	433
tat	ggg	aca	att Ile	מננ	ggc	Lou	m	Dha	Lon	DYA	Dro	Coc	Ser	Acr	Thr	255
ıyr	чтУ	THE	тте	776	GTĀ	nan	TAT	TITE	TIENT	EIU	-10	202	2001	*		

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

atg ttg
Met Leu

<210> 326

<211> 162

<212> PRT

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820

<400> 326

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser 1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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<210> 327
<211> 475
<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(475)
<223> Taxon = 9600; gene = PPY119; pseudogene; Accession DDBJ/EMBL/GenBank =
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                                                                    120
gtaagettge cettetgtgg cecaaacata gtggacagtt attattgega cettaetttg
gtcatcaaac gtgcctgtac agatgcttat atccctgaag tgttgatgct tttggacggt
ggtcttatgg gggtgaccat ttttgctttt gctgatctcc tacacggtca ttctgattac
tgtgcagcga cattcctcag caggtatggc caaggctcac agcactctga ctgcccacat
tgctgtggtg accgtgttct ttgggccctg tatcttcatc tatgcctggc ctttcagcaa
cttaccagtg gataacattt tgtctgtatt ctctgtagtt ttcacaccta tatta
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<212> DNA
<213> Pongo pygmaeus
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9600; gene = PPY120; Accession DDBJ/EMBL/GenBank = AF179822
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
<400> 328
t gtg gcc atc tgt cac cct cta cat tat gcc acc acc atg agt cag agc
  Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Thr Met Ser Gln Ser
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cag Gln	tgt Cys	gtc Val	atg Met 20	ctg Leu	gtg Val	gct Ala	Gly ggg	tcc Ser 25	tgg Trp	gtc Val	atc Ile	gct Ala	tgt Cys 30	gcg Ala	tgt Cys	97
gct Ala	ctt Leu	ttg Leu 35	cat His	acc Thr	ctc Leu	ctt Leu	ctg Leu 40	gcc Ala	cgg Arg	ctt Leu	tcc Ser	ttc Phe 45	tgt Cys	gct Ala	gac Asp	145
cac His	atc Ile 50	atc Ile	cct Pro	cac His	ttc Phe	ttc Phe 55	tgc Cys	gac Asp	ctt Leu	ggt Gly	gcc Ala 60	ctg Leu	ctc Leu	aag Lys	ctg Leu	193
tcc Ser 65	tgc Cys	tca Ser	gac Asp	acc Thr	tcc Ser 70	ctc Leu	aat Asn	cag Gln	tta Leu	gca Ala 75	atc Ile	ttt Phe	aca Thr	gca Ala	gga Gly 80	241
ttg Leu	aca Thr	gcc Ala	att Ile	atg Met 85	ctt Leu	cca Pro	ttc Phe	ctg Leu	tgc Cys 90	atc Ile	ctg Leu	gtt Val	tct Ser	tat Tyr 95	ggt Gly	289
cac His	att Ile	Gly	gtc Val 100	acc Thr	atc Ile	ctc Leu	cag Gln	att Ile 105	ccc Pro	tcc Ser	acc Thr	aag Lys	ggc Gly 110	ata Ile	tgc Cys	337
aaa Lys	gcc Ala	ttg Leu 115	tcc Ser	act Thr	tgt Cys	gga Gly	tcc Ser 120	cac His	ctc Leu	tca Ser	gtg Val	gtg Val 125	act Thr	atc Ile	tat Tyr	385
tat Tyr	ggg Gly 130	Thr	att Ile	att Ile	ggt Gly	ctc Leu 135	tat Tyr	ttt Phe	ctt Leu	ccc Pro	cca Pro 140	Ser	agc Ser	aac Asn	acc Thr	433
aat Asn 145	Asp	aag Lys	aac Asn	ata Ile	att Ile 150	Ala	tca Ser	gtg Val	ata Ile	tac Tyr 155	Thr	gta Val	gtc Val	act Thr	ccc Pro 160	481
_	ttg Leu															487
	•					,										
<21	.1>	329 162														
	.2> .3>	PRT Pong	yg oy	gmae	us											
<22 <22		misc	_fea	ture	•											
<22	2>	(1).	. (48	37)					_				/ maen-	10-	.Da1-	→ λ⊡170022
<40	0>	329														= AF179822
Val 1	. Ala	ı Ile	е Суя	His 5	Pro	Let	His	тут	Ala 10	Thr	Thr	Met	: Ser	: Glr 15	. Ser	

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly 85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 330

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 330

WO 01/46262	329	PCT/IB00/02017
t gtt gcc ata tgt tac cct ct Val Ala Ile Cys Tyr Pro Le 1 5	c cac tac act gcc atc atg eu His Tyr Thr Ala Ile Met 10	agg gaa ggg 49 Arg Glu Gly 15
ctc tgt gcc ttc tta gtg gct Leu Cys Ala Phe Leu Val Ala 20	gta tct tgg att cca tct tc Val Ser Trp Ile Pro Ser C 25	s Ala Ser
tcc ctc tct cac acc ctt ctg Ser Leu Ser His Thr Leu Leu 35	ctg acc ccg ctg cct ttc t Leu Thr Pro Leu Pro Phe C 40 45	gt gat gca 145 ys Asp Ala

aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu

50 55 60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg

100 105 110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat

1385

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr

115

120

125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser

130 135 140

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro

150 155 160

atg ctg
Met Leu

<210> 331

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<400> 331

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140

Met Leu

<210> 332

<211> 488

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9521; gene = SSC185; Accession DDBJ/EMBL/GenBank = AF179824

<220>

<221> CDS

VV O 01/40202		331	
<222> (2)(487 <223> Product = <400> 332	olfactory recep		40
t gtt gcc ata tg Val Ala Ile Cy 1	gt tac cct ctc cays Tyr Pro Leu H: 5	ac tac act gcc atc at is Tyr Thr Ala Ile Me 10	g agg gaa ggg 49 et Arg Glu Gly 15
ctc tgt gcc ttc Leu Cys Ala Phe 20	tta gtg gct gta Leu Val Ala Val	tct tgg att cca tct Ser Trp Ile Pro Ser 25	tgt gct agc 97 Cys Ala Ser 30
tcc ctc tct cac Ser Leu Ser His 35	acc ctt ctg ctg Thr Leu Leu Leu 40	acc ccg ctg tct ttc Thr Pro Leu Ser Phe 45	tgt gat gca 145 Cys Asp Ala
aac acc gtc cac Asn Thr Val His 50	cac tac ttc tgt His Tyr Phe Cys 55	gac ctt gct gcc ctg Asp Leu Ala Ala Leu 60	ctc aag ctg 193 Leu Lys Leu
tcc tgc tca gat Ser Cys Ser Asp 65	atc ttc ctc aac Ile Phe Leu Asn 70	gag ctg gtc atg ttc Glu Leu Val Met Phe 75	aca gta ggg 241 Thr Val Gly 80
gtg gtg gtc att Val Val Val Ile	acc ctg cca tto Thr Leu Pro Phe 85	e atg tgt atc ctg gta Met Cys Ile Leu Val 90	tca tat ggc 289 Ser Tyr Gly 95
tac act ggg gcc Tyr Thr Gly Ala 100	Thr Ile Leu Arg	g gtc cct tca acc aaa g Val Pro Ser Thr Lys 105	ggg atc cgc 337 Gly Ile Arg 110
aaa gcg ttg tcc Lys Ala Leu Ser 115	e atg tgt ggc tcc Met Cys Gly Ser 120	c cgt ctc tct gtg gtg r Arg Leu Ser Val Val) 125	Ser Leu Tyr
tat ggc tca ata Tyr Gly Ser Ile 130	a ttt ggc cag tag e Phe Gly Gln Ty 135	c ctt ttc cca act gta r Leu Phe Pro Thr Val 140	agc agt tcc 433 Ser Ser Ser
att gac aag gat Ile Asp Lys Asr 145	t gtc att gtg gc o Val Ile Val Al 150	t cta atg tac aca gtg a Leu Met Tyr Thr Val 155	g gtc aca ccc 481 L Val Thr Pro 160
atg ctg t Met Leu			488

<210> 333 <211> 162 <212> PRT <213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9521; gene = SSC185; Accession DDBJ/EMBL/GenBank = AF179824

<400> 333

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35 40 45

Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

<210> 334

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

PCT/IB00/02017 WO 01/46262 333 <223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825 <220> <221> CDS <222> (2)..(487) <223> Product = olfactory receptor <400> 334 t gtg gcc act tgt cac ccc ctt aga tac atg gtc atc atg aac ccc tgc 49 Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys 5 97 ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn 20 25 gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat 145 Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp 35 . 40 ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu 50 55

241

65			70			75			80	
			gtt Val							289
			att Ile							337
			tgt Cys							385
			ggg Gly							433
			gtg Val 150							481
atg	gtg									487

gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala

<210> 335 <211> 162 <212> PRT

Met Val

PCT/IB00/02017 WO 01/46262 334

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<400> 335

Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys

Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn 25

Ala Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp 40

Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu 60 55 50

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala 75 70

Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala 90

Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr 100

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe 120 115

Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser 135 130

Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln 150 155 145

Met Val

<210> 336

<211> 487

<212> DNA

<213> Saimiri sciureus

<220> <221> misc_feature													
<222> (1)(487)													
<pre><223> Taxon = 9521; gene = SSC187; Accession DDBJ/EMBL/GenBank = A</pre>	F179826												
<220>													
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<222> (2)(487)													
<pre><223> Product = olfactory receptor</pre>													
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met													
1 5 10 15													
,													
ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat	97												
Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His													
20 25 30													
gec atg ttg cac act tta ctc atg gcc agg ttg cgt ttt tgt gca gac	145												
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp													
35 40 45													
aat gtg atc ctc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg	193												
Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 60													
50 55 60													
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga	241												
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly													
65 70 75 80													
	200												
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca	289												
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85 90 95													
03													
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc	337												
Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys													
100 105 110													
aag goo gto tot act tgt ggo too cac etc tot gtg gtg toa ctg tto	385												
Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe	505												
115 120 125													
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct	433												
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser													
130 135 140													
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc	481												
Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro													
145 150 155 160													
	400												
atg ctg	487												
Met Leu													

PCT/IB00/02017 WO 01/46262

<210> 337

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC187; Accession DDBJ/EMBL/GenBank = AF179826

<400> 337

Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met 10 . 15 5 1

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25 20

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp 35 40

Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 105

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120 115

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 135 130

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 150 155

Met Leu

							•		33	′						
<211>	- 4	87														
<212>	ם	NA														
<213>		aimi	ri s	ciur	eus											
<220>																
<221>		_	feat													•
<222>			(487				0001	00.	3000	oaio	∽ DE	ND T / E	MET.	ConB	ank -	λ ₽170 Ω27
<223>		axon	. = 9	521;	gen	e =	SSCI	.90;	ACCE	8510	וו טב	/DU / E	/ درمین	Gene	allk -	AF179827
<220><221>		DS														
<222>			(487	١,												
<223>			ict =		acto	rv r	ecer	tor								
<400>		38				_	-									
t gtg	g gc	c at	c tg	t aa	g cc	c ct	g ca	it ta	ac ac	c ac	c at	c at	gag	rc ag	c aaa	49
Va]	L Al	a Il	.e Cy	s Ly	s Pr	o Le	u Hi	s Ty			r Il	.e Me	t Se		r Lys	
1				5					10)				15	5	
				_ 1_ 1_				.	L	~	a++	aa+		ata	ata	97
atc t																٥,
TTG (-ys	реп	20	реп	vaı	пеп	GIY	25	ııp	V (1.1	Deu	<u>.</u>	30			
			20										•			•
atc 1	ttt	cca	cca	ctc	ctc	tta	gga	cta	aat	ctt	gac	ttc	tgt	gcc	tcc	145
Ile 1																
		35					40					45				
											•					
aac g																193
Asn '		Val	qzA	His	Phe		Phe	Asp	Thr	тте		ьeu	rea	GIN	TIE	
-	50					55					60					
tcc	tac	202	asc.	aca	can	ctc	cta	gag	agg	ato	gga	ttc	atc	tca	aca	241
Ser																
65	-1 -				70				_	75	_				80	
ttg																289
Leu '	Val	Thr	Leu		Val	Thr	Leu	Val		Val	Ile	Ile	Ser		Thr	
				85					90					95		
tat			_ • - •							+	200	204	~~~	200		337
tat Tyr																,,,
ıyı	TTE	АТа	100	1111	116	neu	ny 5	105	110	DCI	****	501	110	9		
			200													
aag	gct	ttt	tcc	acg	tgt	tct	tct	cac	atg	att	gtg	ata	tcc	ctt	tct	385
Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Met	Ile	Val	Ile	Ser	Leu	Ser	
		115					120					125				
				•												422
tat	ggc	agc	tgc	atc	ttc	atg	tat	gtt	aag	cca	tca	gtc	aaa	caa	agg	433
Tyr		Ser	Cys	Ile	Phe		Tyr	Val	Lys	Pro	Ser		гĀЗ	GIN	Arg	
	130					135					140					
a+=	tct	+++	tca	aac	dus	att	ton	ata	ctc	aat	acc	tet	att	act	cca	481
Val																
145				-1-	150					155					160	
ctt	ttg															487
Leu	Leu															

<210> 339

<211> 162

<212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC190; Accession DDBJ/EMBL/GenBank = AF179827

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys

Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile 25

Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser 40

Asn Val Val Asp His Phe Tyr Phe Asp Thr Ile Pro Leu Leu Gln Ile 55

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala 70

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr 90

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys 105 100

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser 120 115

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg 130 135

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro 160 150 145

Leu Leu

4

PCT/IB00/02017 WO 01/46262 339

<223>	CDS (1). Prod	_feat .(485 n = 9	ure) 521;)	gen				Acce	ssio	n DD	BJ/E	MBL/	GenB	ank =	AF179828
<400> gtg gc Val Al 1	c att	tgc Cys	cac His 5	cct Pro	ctt Leu	caa Gln	tac Tyr	tca Ser 10	gtc Val	atc Ile	atg Met	acc Thr	aca Thr 15	ggt Gly	48
tac tg Tyr Cy	ıt gga vs Gly	cag Gln 20	ctg Leu	gtg Val	gct Ala	ttc Phe	tct Ser 25	tac Tyr	atg Met	agt Ser	ggt Gly	ttc Phe 30	atg Met	atc Ile	96
tct gt Ser Va	c atc al Ile 35	aag Lys	gtc Val	tat Tyr	ttc Phe	att Ile 40	tca Ser	cat His	gtt Val	gct Ala	ttc Phe 45	tgt Cys	ggc Gly	tcc Ser	144
aat gt Asn Va	al Met	aac Asn	cac His	ttt Phe	ttc Phe 55	tgt Cys	gat Asp	atc Ile	tca Ser	cca Pro 60	gtc Val	cta Leu	aaa Lys	ctg Leu	192
gca to Ala Cy 65	ys Lys	gac Asp	atg Met	tcc Ser 70	aca Thr	gct Ala	gag Glu	cta Leu	gtg Val 75	gac Asp	ttt Phe	gct Ala	tta Leu	gct Ala 80	240
atc gi	tc att al Ile	ctt Leu	gtg Val 85	atc Ile	cct Pro	ctc Leu	att Ile	acc Thr 90	act Thr	atc Ile	ctc Leu	tcc Ser	tat Tyr 95	atc Ile	288
tac a Tyr I	tt gto le Val	tcc Ser 100	gcc Ala	att Ile	ctg Leu	cat His	ata Ile 105	ccc Pro	tcc Ser	acc Thr	cag Gln	gga Gly 110	agg Arg	aag Lys	336
aag g Lys A	cc tto la Phe 11	e Ser	acc Thr	tgt Cys	gca Ala	tct Ser 120	cac His	ctc Leu	act Thr	gta Val	gtc Val 125	ata Ile	att Ile	ttt Phe	384
Tyr T	ca gco hr Ala 30	atg Met	att Ile	ttt Phe	aca Thr 135	tat Tyr	gtt Val	cgg Arg	ccc Pro	aga Arg 140	Ala	att Ile	gca Ala	tca Ser	432
	at to									Ala					480

PCT/IB00/02017 WO 01/46262

atg ct Met

485 .

<210> 341 <211> 161 <212> PRT

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF179828

<400> 341

Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly 1 5 10

Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile 25 30

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser

Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu 50 . 55 60

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala 75 70

Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile

Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 105 100

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 120

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 135

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro 150 155

Met

<210> 342	
<211> 487	
<212> DNA	
<213> Saimiri sciureus	
<220>	
<221> misc_feature	
<222> (1)(487)	70020
<223> Taxon = 9521; gene = SSC192; Accession DDBJ/EMBL/GenBank = AF1	19049
<220>	
<221> CDS	
<222> (2)(487)	
<223> Product = olfactory receptor	
<400> 342	49
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Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly	
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ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc	97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser	
20 25 30	
20 23	
tee etc tet cae ace ett etg etg ace eeg etg tet tte tgt gat gea	145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala	
35 40 45	
33	
aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg	193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu	
50 55 60	
•	
tee tge tea gat ate tte ete aat gag etg gte atg tte aca gta ggg	241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly	
65 70 75 80	
gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc	289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly	
85 90 95	
tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc	337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg	
100 105 110	
	205
aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat	385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr	
115 120 125	
	422
tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc	433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser	
130 135 140	

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

481

487

Met Leu

<210> 343
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<212> PRT
<213> Saimiri sciureus
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Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130

The Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

•															•
<210>	344														
<211>	487														
<212>	DNA														
<213>	Sain	iri s	ciur	eus											
<220>															
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<223>	Tax	n = 9	521;	gene	9 = 5	SSCI	93; 1	Acce	SSIO	עע ז.	50 / E	٠١٠٠٠	احتبيات		F179830
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<221>	CDS														
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<223>		uct =	. OII	acto.	ry r	ecep	COL								
<400> t gtt	344			a ac	+ c+	c ca	c ta	c ac	t ac	c at	c at	a aa	g ga	a ggg	· 49
t gtt	gcc i	ita c	ji ta 10 Th	r Dr	o Tiel	n Hi	s Tv	r Th	r Al	a Il	e Me	t Ar	g Gl	u Gly	
	ALA .	rie C	, s <u>1 y</u> 5	T F1	O De	u	J -3	10			_		_ 15	_	
1			,												
ctc to	** ~~	- +tc	tta	ata	act ·	ota	tct	taa	att	cca	tct	tgt	gct	agc	97
Leu Cy	re Al	Phe	Leu	Val	Ala '	Val	Ser	Trp	Ile	Pro	Ser	Cys	Ala	Ser	
neu cy	'S LT	20					25	-				30			
tcc c	ta ta	t cac	acc	ctt	ctg	ctg	acc	ccg	ctg	tct	ttc	tgt	gat	gca	.145
Ser Le	eu Se	r His	Thr	Leu	Leu	Leu	Thr	Pro	Leu	Ser	Phe	Cys	Asp	Ala	
	35					40					45				
aac a	cc gt	c cac	cac	ttc	ttc	tgt	gac	ctt	gct	gcc	ctg	ctc	aag	ctg	193
Asn T	hr Va	l His	His	Phe	Phe	Cys	Asp	Leu	Ala	Ala	Leu	Leu	Lys	Leu	
5					55					60					
															241
tcc t	gc to	a gat	atc	ttc	ctc	aat	gag	ctg	gtc	atg	ttc	aca	gta	999	241
Ser C	ys Se	r Asp	Ile	Phe	Leu	Asn	Glu	Leu	Val	Met	Pne	Thr	vai	GTA	
65				70					75					80	
											~+~	+ ==	+=+	aac	289
gtg g	tg gt	c att	acc	ctg	cca	ttc	atg	tgt	atc	ctg	gra 1701	Cor	Tur	Glv	203
Val V	al Va	il Ile		Leu	Pro	Phe	Met		TTE	Leu	Val	Ser	95	GTA	
			85					90	•				90		
									+02	200	222	aaa	atc	cac	337
tac a	ict g	gg gco Ly Ala	acc	atc	ctg	agg	บาไ	Dro	Cor	Thr	Lvs	Glv	Tle	Ara	
Tyr 1	inr G.			TIE	ьeu	ALG	105		261	****	,	110			
		100	,				100								
	+	tg tc			~~~	too	cat	ata	tet	ata	ata	tct	cta	tat	385
aaa g	gcg t	eu Se:	. Mot	Cyc	Glaz	Ser	Ara	Ten	Ser	Val	Val	Ser	Leu	Tyr	
ràs t			. met	. cys	стх	120		u			125			-	
	Т	15				J. 20 ()									
4 ~4~		ca at	<u>.</u> +++		cac	tac	ctt	tto	. cca	act	gta	ago	agt	tcc	433
tat	yyc c	la al	a 666	. ggc	cug						-	_	_		

344 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser 130 135 att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro 150 155 487 atg ctg Met Leu <210> 345 <211> 162 <212> PRT <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830 <400> 345 Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly 10 5 Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser 30 25 Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu 55 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly 75 70 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly 90 95 85 Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg 105 100

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr

120

125

130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro 145 150 150 160

Met Leu

<222> <223> <220> <221> <222> <222> <223>	CDS (2)	feat (486 = 9	ure) 521;	gen		Acce	ssio	n DD	· BJ/E	:MBL/	GenE	ank =	AF179831
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ctg tg Leu Cy													97
tcc tc Ser Se													145
ttg ga Leu Gl 50	u Ile												193
gcc to Ala Cy 65													241
atg ct Met Le													289
aag at Lys II													337
aag go Lys A													385

W	O 01	/4626	2 .						34	6					PCT/IB00/02017		
	;	115					120					125					
tat g Tyr G	gt Sly '	aca Thr	ctc Leu	cta Leu	ggt Gly	gtg Val 135	tac Tyr	att Ile	agt Ser	tct Ser	gct Ala 140	gca Ala	act Thr	ggc Gly	aac Asn	433	
tca o Ser H	at Iis	tca Ser	agt Ser	gct Ala	gca Ala 150	gcc Ala	ttg Leu	gtg Val	atg Met	tac Tyr 155	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro 160	481	
atg (Met	et															486	
<210: <211: <212: <213: <220: <221: <222: <223: <400: Val:	> 1 > F > S > 7 > 7	aimi isc_ (1)	_fea . (48 n =	ture 6) 9521	; ge:											= AF179831	
Leu	Cys	Gly	Leu 20	Leu	Val	Leu	Ala	Ser 25	Trp	Ile	Leu	Ser	· Ala	Leu	. Asn		
Ser	Ser	Leu 35	Gln	Thr	Leu	. Ile	Val 40	Lev	ı Arg	, Leu	Ser	Phe 45	e Cys	Thr	Asp		
Leu	Glu 50	Ile	Pro	His	Ph∈	Phe 55	: Cys	Glu	ı Lev	ı Asr	Glr 60	ı Val	l Ile	His	: Leu		
Ala 65	Cys	Туг	As <u>ı</u>	Th:	70	e Lev	ı Asn	. Ası	o Val	L Va] 75	L Met	Ty:	c Le	ı Ala	a Ala 80		
Met	Leu	Leu	ı Gly	/ Gly 85	/ Gly	y Pro	o Lev	ı Th	r Gly 90	y Ile	e Ile	е Ту	r Se:	r Ty: 95	r Ser		
Lys	Ile	e Val	l Se:	_	r Ile	e Arg	g Ala	11 10		r Se:	r Ala	a Gl	n Gl		s Tyr		
Lys	Ala	11:		r Th	r Cy	s Al	a Sei 120		s Il	e Le	u Il	e Va 12		r Le	u Phe		

Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn 135 130 Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 155 150 Met <210> 348 <211> 487 <212> DNA <213> Saimiri sciureus <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832 <220> <221> CDS <222> (2)..(487) <223> Product = olfactory receptor <400> 348 c gtg gcc atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag 49 Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg 97 Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly 25 gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145 Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 40 35 aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193 Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu 55 50 tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg 241 Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 75 70 289 gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 95 90 85 ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct 337

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser

100

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc 385 Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 120 115 ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc 433 Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 135 140 130 ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc 481 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 155 150 487 atg ttt Met Phe

<210> 349
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<212> PRT
<213> Saimiri sciureus
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Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly 20 25 30

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 35 40 45

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu 50 55 60

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 65 70 75 80

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 85 90 95

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 145 150 155 160

Met Phe

<210> 350 <211> 486 <212> DNA <213> Saimiri boliviensis <220> <221> misc_feature <222> (1)..(486) <223> Taxon = 27679; gene = SBO213; pseudogene; Accession DDBJ/EMBL/GenBank = AF179833 <400> 350 cgtggccatc tgccaccctc tccactatcc catccgcatg agtagaagtg tgtgtgtgaa 60 gatgattgga ggetettgga egetggggte cateaactee ttggcacaca cagtetatge 120 cetecatatt ecetactgea ggtetagage cattgaccat ttettetgeg acateceage 180 catgttgctt ctcgcctgta cggacacttg ggtctatgaa tacatggttt ttctaagtac 240 aagetgeett eteetettte ttteettgge ateacegett eetatggeeg agteetattt 300 gctgtctacc atacgcattc aaaaaaggga agaaaaaagg cctccaccac catttcaacc catttaactg tagtgatett ttactatgca cettttgtet acacetatet teggeceagg 420 aatotocact caccatocga agacaagato otggoagtot totacaccat cottaccoct 480 486 atgctc

<210> 351

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

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<222			(487)												
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<400		51				-	_								•	
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atc	tac	cta	caq	ctt	gtg	ctt	ggg	tgc	tgg	gtt	ctt	ggt	ttt	ctc	atc	97
Tle	Cvs	Leu	Gln	Leu	Val	Leu	Gly	Cys	Trp	Val	Leu	Gly	Phe	Leu	Ile	
	-1-		20				•	25					30			
						•										
atc	ttt	cca	cca	ctc	ctc	tta	gga	cta	aat	ctt	gac	ttc	tgt	gcc	tcc	145
Tle	Phe	Pro	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Leu	Asp	Phe	Cys	Ala	Ser	
116		35					40					45				
	•	JJ														
225	~+ a	~++	ra t	cat	ttc	tac	tat	gac	act	atc	ccq	ctc	ctg	cag	att	193
3	y	77-1) en	Hie	Phe	Tyr	Cvs	Asp	Thr	Ile	Pro	Leu	Leu	Gln	Ile	
ASII		Val	nsp	1113	1110	55	0,70				60					
	50					33				•				•		
			~~~	200	~~	ctc	cta	αaα	agg	ato	aga	ttc	atc	tca	aca	241
tcc	tgc	aca	gac	acy	Clay	LON	Len	Glu	Arg	Met	Glv	Phe	Ile	Ser	Ala	
	Cys	Thr	Asp	THE		Deu	Beu	Giu	, arg	75	1				80	
65					70					, ,						
									-+~	a+ a	a+=	2+2	tra	tat	act	289
ctg	gtg	aca	ctc	tta	gtc	aca	ttg	gta	atg	gra	TIO	Tla	Cor	There	Thr	203
Leu	Val	Thr	Leu		Val	Thr	ьeu	var	Met	Val	TTE	116	Ser	95	1111	
				85					90					93		
															222	337
tat	att	gcc	ctg	aca	att	cta	aaa	atc	cct	tca	act	agt	cag	ayy	aaa Ta	337
Tyr	Ile	Ala	Leu	Thr	Ile	Leu	Lys		Pro	Ser	Thr	ser	GIN	Arg	пĀг	
			100					105					110			
																205
aag	gct	ttt	tcc	acg	tgt	tct	tct	cac	atg	att	gtg	ata	tcc	CLL	ECT	385
Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Met	Ile	Val	Ile	ser	Leu	Ser	
		115					120					125				
tat	ggc	ago	tgc	atc	tto	atg	tat	gtt	aag	cca	tca	gtc	aaa	caa	agg	433
Tyr	Gly	Ser	Cys	Ile	Phe	Met	Tyr	· Val	Lys	Pro	Ser	Val	Lys	Gln	Arg	
_	130					135	,				140					
σta	tct	ttt	tca	aag	gga	att	tcg	gto	rcto	aat	acc	tct	gtt	gct	cca	481
Val	Ser	Phe	Ser	Lys	Gly	, Ile	Ser	· Val	. Leu	Asn	Thr	Ser	Val	Ala	Pro	
145				-	150			٠		155					160	
ctt	: ttg	•														487
	. Lev															
		-														

<210> 352

<211> 162

<212> PRT

PCT/IB00/02017 WO 01/46262 351

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SB0214; Accession DDBJ/EMBL/GenBank = AF179834

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Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile 25

Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser 45 40

Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile 55

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala 75 70

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr 90

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys 100 105

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser 125 120 115

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg 135 130

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro 155 145

Leu Leu

<210> 353

<211> 487

<212> DNA

<213> Saimiri boliviensis

352

332												
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Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser 1 10 15												
att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 20 25 30												
gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro 35 40 45												
tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 50 55 60												
gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att ttg ggt Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 65 70 75 80												
ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct tac gta Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val 85 90 95												
ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg agg ctc Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu 100 105 110												
aag too tto too acg tgt got too cac gto act gtg gto acc atg tto 1385 120 125 126 385												
tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 130 135 140												
cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc tct gcc Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala 145 150 155 160												
ttc ttg Phe Leu												

<210> 354

<211> 162

<212> PRT

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835

<400> 354

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Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly 25

Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro 35

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu 55 50

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly 75 70

Phe Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val 90

Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu 110 105 100

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe 120

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp 135 140

Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala 155 145 150

Phe Leu

354

334													
<211> 487													
> DNA													
<213> Saimiri boliviensis													
<220> <221> misc_feature													
<222> (1)(487)													
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1 5 10 15													
gcc tgc atg acc atg gtg ggc acc tcc tgg ctc aca ggc atc atc aca	97												
Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr													
. 20 25 30													
gcc acc acc cat gcc tcc ctc atc ttc tct ctg ccc ttc ccc agc cac	145												
Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His													
35 40 45													
	193												
cca atg atc cca cac ttt ctc tgt gac atc ctg cca gta ctg aga ctg Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu	133												
50 55 60													
30 33													
gca agt gct ggg aag cac agg agt gag atc tcc gtg atg aca gct acc	241												
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr													
65 70 75 80													
gta gtc ttc atc atg gtc cct ttc tct atg att gtc acc tct tac atc	289												
Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile													
90 95													
	227												
ege ate etg ggt gee ate eta gea atg act tee ace cag age ege cae	337												
Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His 100 105 110													
100 103													
aag gtc ttc tcc acc tgc tcc tcc cat ctg ctt gtg gtc tgt ctc ttc	385												
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe													
115 120 125													
ttt gga aca gcc agc atc acc tac ata cgg ccc cag gca ggc tcc tct	433												
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser													
130 135 140													
gtc acc aca gac cgc atc ctc agt ctc ttc tac acg gtc atc aca ccc	481												
Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro													
145 150 155 160													
atg ctc	487												
Met Leu													

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<210> 356

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<213> Saimiri boliviensis

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<222> (1)..(487)

<223> Taxon = 27679; gene = SB0216; Accession DDBJ/EMBL/GenBank = AF179836

<400> 356

Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Gln

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15

Ala Cys Met Thr Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr 20 25 30

Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Pro Ser His 35 40 45

Pro Met Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu 50 55 60

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr 65 70 75 80

Val Val Phe Ile Met Val Pro Phe Ser Met Ile Val Thr Ser Tyr Ile 85 90 95

Arg Ile Leu Gly Ala Ile Leu Ala Met Thr Ser Thr Gln Ser Arg His
100 105 110

Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Cys Leu Phe 115 120 125

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser 130 135 140

Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro 145 150 155 160

Met Leu

PCT/IB00/02017 WO 01/46262 356

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<220																
<221			feat													
<222			(487													
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<220																
<221		DS														
			(487													
			ict =	olf	acto	ry r	ecer	otor								
<400																
										er Th					c caa o Gln	49
	LL				~+~					a+ a	a+ a	200	224	~++	~++	97
			cta Leu													31
vai	cys	Ala	20	TIE	Dea	val	neu	25	тър	val	neu	1111	30	vaı	vai	
			20					2,5					50			
acc	tta	200	cac	aca	ctc	ctc	ato	act	cga	cta	tee	ttc	tat	ata	act	145
			His													
ALU	БСС	35		****			40		9			45	0,72			
		72														
aaa	даа	att	gct	cac	ttt	ttc	tat	gac	atc	act	cct	atc	cta	aaσ	cta	193
	_		Ala													
1	50					55	-				60			-		
	•															
tca	tgt	tct	gac	acc	cac	atc	aat	gag	atg	atg	gtt	ttt	gtc	ttg	gga	241
			Asp													
65	_		_		70					75					80	
			ctc													289
${ t Gly}$	Thr	Val	Leu	Ile	Ile	Pro	Phe	Leu	Cys	Ile	Val	Thr	Ser	Tyr	Ile	
				85					90					95		
			cct	-		_										337
Tyr	Ile	Val	Pro	Ala	Ile	Leu	Arg		Arg	Thr	His	Gly		Ala	Gly	
			100				•	105					110			
																205
			tcc													385
Lys	Ala		Ser	Thr	Cys	ser		His	ьeu	Cys	тте		Cys	vaı	Phe ·	
		115					120					125				
L 1						~	.	a b c	h	act			26-		tat	433
			ctc		_	_		_	_					_		433
TYT	_		Leu	rne	ser		TAL	ьeu	cys	PIO		ser	тте	WIG	ser	
	130					135					140					
~	~~+	224	gac	2++	uu=	802	aat	GO:	a+~	+=+	200	242	a+~	a	ccc	481
			Asp													-01
145	νsħ	nys	roh	776	150	- ***	n_u	******	1166	155			- 41	T11T	160	
エモコ																

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487 acg ttg Thr Leu <210> 358 <211> 162 <212> PRT <213> Saimiri boliviensis <220> <221> misc_feature <222> (1)..(487) <223> Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AF179837 <400> 358 Val Ala Ile Cys His Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln 5 Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val 25 20 Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr 40 35 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu 50 55 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly 70 75 Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile 90 95 85 Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly 105 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe 120 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser 135 130 Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro

155

150

Thr Leu

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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln												
- 10 15												
1 5 10 15												
gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg	7											
Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly												
20 25 30												
gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa 145	5											
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu												
35 40 45												
aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc 193	3											
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu												
50 55 60												
	_											
tcc tgc aac age tct tac ata aat ttg ctg ttg gtt ttt att att gtg 24:	1											
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Val Phe Ile Ile Val												
65 70 75 80												
200	٠.											
gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt 289	9											
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly												
85 90 95												
the art too ago att ste cae att age tee aga gag agg tet 33	7											
ttt att ttt ttt age att ete cae att age too aca gas ggo ags	•											
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser												
100 105 110												
and goe the agt acc top age top car ata att gtg gta tog ott tte 38	15											
add gcc ccc age acc ego ago ood add and gra gra and	•											
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 115 120 125												
115 120 125												
ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc 43	13											
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro	-											
400												
130 135 140												

359

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg cca 481 Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro 150

486 tgt tt Cys

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<213> Saimiri boliviensis

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<222> (1)..(486)

<223> Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838

<400> 360

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Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly 20

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu 40

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu 55

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val 75 70

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly 90 85

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser 105 100

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe 120 115

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro 135 140 130

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro

145 150 155 160

Суѕ

<210>	361														
<211>	487														
<212>	DNA														
<213>	•														
<220>															
	T														
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<221>	CDS	//07													
	(2)			acto	m, r	ecen	tor								
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t gtg	20T	·+ +a	r ca	.c. cc	t ct	t ca	a ta	c to	a at	c at	c at	g ac	c ac	a ggt	49
t gtg Val	Ala Il	le Cv	s Hi	s Pr	o Le	u Gl	n Tv	r Se	r Va	1 Il	e Me	t Th	x Th	r Gly	
1	nia i		5				4	10					15	;	
-			_												
tac tg	t aga	caq	ctg	gtg	gct	ttc	tct	tac	atg	agt	ggt	ttc	atg	atc	97
Tyr Cy	s Gly	Gln	Leu	Val	Ala	Phe	Ser	Tyr	Met	Ser	Gly	Phe	Met	Ile	
-4 4	-	20					25					30			
tct gt	c atc	aag	gtc	tat	ttc	att	tca	cat	gtt	gct	ttc	tgt	ggc	tcc	145
Ser Va	l Ile	Ьуs	Val	Tyr	Phe	Ile	Ser	His	Val	Ala		Суз	Gly	Ser	
	35					40					45				
															102
aat gt	t atg	aac	ctc	ttt	ttc	tgt	gat	atc	tca	cca	gtc	cta	aaa	ctg	193
Asn Va		Asn	Leu	Phe		Cys	Asp	ITE	ser		val	ьеп	гуѕ	Leu	
50)				55					60					
				L			~-~	at a	a+a	as c	+++	act	tta	act	241
gca to	gc aaa	gac	Mob	CCC	mb~	yc.	Glu	T.e.ii	Wal	Asn	Phe	Ala	Leu	Ala	
	үз ьуз	Asp	Met	70	TIII	MIG	GIU	Dea	75	nop				80	
65				70					, 5						
atc g	ta att	att	ata	atc	cct	ctc	att	acc	act	atc	ctc	tcc	tat	atc	289
Tlo W	al Ile	T.ell	Val	Tle	Pro	Leu	Ile	Thr	Thr	Ile	Leu	Ser	Tyr	Ile	
TIE A	ar ire	. Deu	85					90					95		
			-												
tac a	tt gto	tcc:	acc	att	ctq	cat	ata	ccc	tcc	acc	cag	gga	agg	aag	337
Tvr I	le Val	Ser	Ala	Ile	Leu	His	Ile	Pro	Ser	Thr	Gln	Gly	Arg	Lys	
-3		100			•		105					110			
aag q	cc tto	tcc	acc	tgt	gca	tct	cac	ctc	act	gta	gto	ata	att	ttt	385
Lys A	la Phe	e Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	Phe	
_	115					120					125				
															422
tac a	.ca gc	atg	att	ttt	aca	tat	gtt	. cgg	CCC	aga	gct	att	gca	tca	433

3

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser 130 135 140

ttt aat tcc aac aaa cta atc tca gct gtc tat gca gtc ctc aca ccc

Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro

145 150 160

atg cta
Met Leu

<210> 362

<211> 162

<212> PRT .

<213> Saimiri boliviensis

<220>

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<222> (1)..(487)

<223> Taxon = 27679; gene = SBO219; Accession DDBJ/EMBL/GenBank = AF179839

<400> 362

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1 5 10 15

Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile 20 25 30

Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser 35 40 45

Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu 50 55 60

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala 65 70 75 80

Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile 85 90 95

Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe 115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser

130 135 140

Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro 145 150 150 155 160

Met Leu

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<210> 363
<211> 488
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
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gettgtgett gggtgetggg ttettggttt teteateate ttteeaceae teetettagg
                                                                    120
actamatctt gacttctgtg cctccaacgt cgttgatcat ttctactgtg acactatccc
                                                                    180
geteetgeag attteetgea cagacaegea geteetggag aggatgggat teateteage
                                                                    240
gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgccct
                                                                    300
gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc
                                                                    360
tcacatgatt gtgatatccc tttcttatgg cagctgccat cttcatgtat gttaagccat
cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc
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                                                                     488
cacttttg
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<210> 364
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<212> DNA

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<222> (2)..(487)

<223> Product = olfactory receptor

<400> 364

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ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 20 25 30	97
gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp 35 40 45	145
aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg. Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 50 55 60	193
gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 65 70 75 80	241
ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85 90 95	289
cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110	337
aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 115 120 125	385
tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 130 135 140	433
act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 145 150 155 160	481
atg ctg Met Leu	487
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<223> Taxon = 27679; gene = SBO221; Accession DDBJ/EMBL/GenBank = AF179841
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Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met 5

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His 25

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp 40

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu 55 50

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly 70 65

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala 85

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys 100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe 120

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser 140 130

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro 150

Met Leu

<210> 366

<211> 487

<212> DNA

<213> Saimiri boliviensis

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<222> (1)..(487)

<223> Taxon = 27679; gene = SBO222; Accession DDBJ/EMBL/GenBank = AF179842

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c gt	g go	c at								t Va					c cag co Gln	49
		ttg Leu														97
gct Ala	gtg Val	gct Ala 35	cat His	aca Thr	gga Gly	aat Asn	ata Ile 40	gtg Val	ttt Phe	cta Leu	acc Thr	ttt Phe 45	tgt Cys	gca Ala	Gly	145
		gtc Val														193
		aat Asn														241
		ggc														289
		ctt Leu														337
		ttc Phe 115														385
															ccc Pro	433
	Asp										Thr				ccc Pro 160	481

487

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atg ttt Met Phe

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SB0222; Accession DDBJ/EMBL/GenBank = AF179842

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Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly 25

Ala Val Ala His Thr Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Gly 40

Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu 55

Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val 70

Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly 85

Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser 105 100

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe 125 120 115

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro 135 140 130

Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro 155 150 145

Met Phe

<210> 368

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

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<222> (1)..(487)

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<222> (2)(487)	
<223> Product = olfactory receptor	
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Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg	
1 5 10 15	
the second of th	97
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat	91
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn 20 25 30	
20 25 30	
the beautiful and the sea of the sea of the tree are green	145
tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp	113
35 40 45	
ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt	193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu	
50 55 60	
50	
gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct	241
Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala	
65 70 75 80	
atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct	289
Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser	
85 90 95	
•	
aag ata gtt too too ata ogt goa ato toa toa got cag ggg aag tac	337
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr	
100 105 110	
aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt	385
Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe	
115 120 125	
	122
tat ggt aca ctc cta ggt gtg tac ctt agt tct gct gca act ggc aac	433
Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn	
130 135 140	
har and har and see see the steepth and and see see see	481
tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro	-0-
145 150 155 160	
747 720 720	
atg ctg	487
Met Leu	
100 200	

<210> 369 <211> 162 368

<212> PRT

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<222> (1)..(487)

<223> Taxon = 27679; gene = SBO223; Accession DDBJ/EMBL/GenBank = AF179843

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Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp 35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu 50 55 60

Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala 65 70 75 80

Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser 85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe 115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn 130 135 140

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro 145 150 155 160

Met Leu

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<211> 649

PCT/IB00/02017 WO 01/46262 369 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank = AF073959 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 370 c ata gct gac atc ggc ttc acc tcc acc act atc ccc aag gtt ctg cag 49 Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln 97 act atc cac aca cag agc aaa ttc atc tct ttc tcg ggc tgc atc aca Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr 25 145 cag ata ttt ttc ttc att gtg ttt gga tgc ctg gac aat tta ctc cta Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu 35 tca gtg atg gcc tat gac cgc ttt gtg gcc atc tgc cat ccc ttg cac 193 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55

tat gtg gtc atc atg aat tct tgc ttc tgt gtg atg ctg gct ctt gga 241

Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly

Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly
65 70 75 80

tca tgg ata gtc agc gtc atg agt tcc cta cct gag acc ttg act gtg

Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val

85 90 95

tta aga cta tcc ttc tgt aca aac atg gaa att cca cac ttt ttc tgt
Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
100 105 110

gat ctt ccc gaa gtc ctg aag ctt gcc tgt tct gac acc ctt gtt aat

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn

115 120 125

aac att gtg aca tat tct ata acc ata gtc ata gct ggt ttc cca ttc

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe

130

135

140

tct ggg att cta ttg tct tat tct aag att ttc tcc tcc atc cta aga

Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg

145

150

150

481

att cet tea get ggg gge aag tac aaa gee ttt tet ace tgt ggg tet 529

PCT/IB00/02017 WO 01/46262 370 Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 cat ctt ttg gtg gtc ttc tta ttc tat agc aat ggt ctt ggg gtc tac 577 His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 185 ctc agc tct gca gcc aca tca tct tct aga atg agt cta gtt gcc tca 625 Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 200 649 ctg atg tac agc ata gtc act ccc Leu Met Tyr Ser Ile Val Thr Pro 210 <210> 371 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank = AF073959 <400> 371 Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr 25 Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu Leu 35 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 55 50 Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly 75 70 Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val

85

100 105

· 90

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn 115 120 125

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe 130 135 140

Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg 145 150 150 155 160

Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr 180 185 185

Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser 195 200 205

Leu Met Tyr Ser Ile Val Thr Pro 210 215

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<212> DNA

<213> Mus musculus domesticus

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<223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank =

AF073960

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<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2

and TM7

<400> 372

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Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln

1 5 10 15

aac atg caa agc caa gtt cca tcc ata ccc tat gca ggt tgc ctg gca

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20 25 30

caa atg tac ttt ttc ctg ctt ttt gca gat ctc gag agc ttc ctc ctt

Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu

35 40 45

gtg gcc atg gcc tat gat cgc tat gtg gcc atc tgc ttc ccc cta cac 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His tat act agc atc atg agc ccc aag ctg tgt ctc tgc ctg gtg gca cta 241 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu 70 289 tet tgg eta etg ace aca gte ate tet ttg tea eac aca etg etc atg Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met 90 get egg etc tec tte tgt get aac aat gtg att eet eac ttt tte tgt 337 Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Phe Cys 105 100 gat atg tca gct ctt ctg aag tta gcc tgc tct gac att cag atc aat 385 Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn 115 120 aag ttg atg ata ttt atc ttg gga gga ctt gtc att att gtc cca ttc 433 Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe 135 130 481 ctg ctg ata ttt tca tcc tat gca cga ata gtg tcc tcc att ctc aag Leu Leu Ile Phe Ser Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 150 145 gtc ccc tct tct aga agc atc cgc aag gcc ttc tcc acc tgt ggt tcc 529 Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 170 165 cac etc tet gtg gtg tet ett tte tat ggg aca ate att ggt etc tat 577 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 tta cgt cca tca gct aat aat tca acc att aag gag act gtc atg gct 625 Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala 205 200 195 649 gtg atg tac acg gtg gtg acc cct Val Met Tyr Thr Val Val Thr Pro 215 210 373 <210> <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649)

<223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank = AF073960

<400> 373

Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Gln 1 5 10 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His . 50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu 65 70 75 80

Ser Trp Leu Leu Thr Thr Val Ile Ser Leu Ser His Thr Leu Leu Met 85 90 95

Ala Arg Leu Ser Phe Cys Ala Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Gln Ile Asn 115 120 120 125

Lys Leu Met Ile Phe Ile Leu Gly Gly Leu Val Ile Ile Val Pro Phe
130 140

Val Pro Ser Ser Arg Ser Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Arg Pro Ser Ala Asn Asn Ser Thr Ile Lys Glu Thr Val Met Ala 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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and	TM7															
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c tt	c to	t ga	t ct	c tg	c tt	t to	c tc	t gt	c ac	a at	g cc	c aa	a tt	g ct	g cag	49
Ph	e Se	r As	p Le	u Cy	s Ph	e Se	r Se	r Va	1 Th	r Me	t Pr	о Гл	s Le	u Le	u Gln	
1				5					10					15		
aac	atg	cag	agc	cag	gac	tca	tcc	atc	acc	tat	gca	gga	tgc	ctg	aca	97
Asn	Met	Gln	Ser	Gln	Asp	Ser	Ser	Ile	Thr	Tyr	Ala	Gly	Суѕ	Leu	Thr	
			20					25					30			
caa	atg	tac	ttt	ttc	ttg	ctc	ttt	gga	gac	ctt	gag	agc	ttc	ctc	ctt	145
Gln	Met	Tyr	Phe	Phe	Leu	Leu	Phe	Gly	Asp	Leu	Glu	Ser	Phe	Leu	Leu	
		35					40					45				
gtg	gcc	atg	gcc	tat	gac	cgc	tat	gtg	gcc	atc	tgc	ttc	ccc	ctt	cat	193
Val	Āla	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His	
	50					55					60					
tac	atg	agc	atc	atg	agc	ccc	agc	ctc	tgt	gtg	agt	ctg	gtg	ctg	ctg	241
Tyr	Met	Ser	Ile	Met	Ser	Pro	Ser	Leu	Cys	Val	Ser	Leu	Val	Leu	Leu	
65					70					75					80	
tcc	tgg	gtg	ctg	acc	act	ttc	cat	gcc	atg	ctg	cat	acc	ctg	ctc	atg	289
Ser	Trp	Val	Leu	Thr	Thr	Phe	His	Ala	Met	Leu	His	Thr	Leu	Leu	Met	
	-			85					90					95		
gcc	aga	ttg	tca	ttc	tgt	gag	gac	aat	gtg	atc	CCC	cac	ttt	ttc	tgt	337
Ala	Arg	Leu	Ser	Phe	Суз	Glu	Asp	Asn	Val	Ile	Pro	His	Phe	Phe	Cys	
													110			
gac	atq	tct	gct	ctg	ctg	aag	ctg	tcc	tgc	tct	gac	act	cac	gtt	aat	385
Asp	Met	Ser	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Thr	His	Val	Asn	
		115				_	120					125				
σаа	tta	ata	ata	ttt	gtc	aca	gga	ggc	ctg	atc	ctt	gtc	att	cca	ttt	433
Glu	Len	Val	Ile	Phe	Val	Thr	Gly	Gly	Leu	Ile	Leu	Val	Ile	Pro	Phe	
	130					135					140					

gtg Val 145	ctc Leu	atc Ile	ctt Leu	gtg Val	tcc Ser 150	tat Tyr	gca Ala	cga Arg	att Ile	gtg Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160	481
gtc Val	ccg Pro	tct Ser	gct Ala	cga Arg 165	ggc Gly	atc Ile	cgt Arg	aaa Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggg Gly 175	tcc Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	gtg Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	GJA aaa	gca Ala	atc Ile	att Ile	ggt Gly 190	ctg Leu	tac Tyr	577
tta Leu	tgt Cys	cca Pro 195	Ser	gct Ala	gat Asp	aac Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gaa Glu	act Thr 205	gtc Val	atg Met	gcc Ala	625
		Tyr		gtg Val												649
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Ası	n Met	: Glr	20	Glr.	a Asp	Ser	Ser	Ile 25	Thr	тух	· Ala	Gly	. Cys	Leu	Thr	
Gl	n Met	: Туз 35		∋ Ph∈	e Lev	. Lev	Phe 40	Gly	As <u>r</u>	o Lev	ı Glu	ser 45	Phe	Lev	ı Leu	
Va	1 Ala 50	a Mei	t Ala	а Туг	c Asp	Arg 55	у Туг	· Val	. Ala	a Ile	e Cys 60	s Phe	e Pro	Let	ı His	
Ту 65		t Se	r Il	e Me	E Sei 70	r Pro	Ser	Leu	і Су	s Va: 75	l Se:	r Lei	ı Val	L Le	ı Leu 80	ı
Se	r Tr	p Va	l Le	u Th 85	r Th	r Phe	e His	s Ala	а Ме 90		u Hi	s Thi	r Lei	ı Le	u Met	:

85

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 115 120 120

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 130 135 140

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 195 200 205

Met Met Tyr Thr Val Val Thr Pro 210 215

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<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

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<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

1 5 10 15

aat atg cag agc cag gac cca tcc atc ccc tat gga ggt tgc ctg gca 97
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala
20 25 30

					atg	att	+++	aaa	gac	ato	gaa	age	ttc	ctt	ctt	1	145
Gln	Ile	Phe 35	Phe	Phe	Met	Leu	Phe 40	Gly	Asp	Met	Glu	Ser 45	Phe	Leu	Leu		
gta Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctg Leu	cat His	;	193
tac Tyr 65	act Thr	agc Ser	atc Ile	atg Met	agt Ser 70	cct Pro	aag Lys	gtc Val	tgt Cys	act Thr 75	ttt Phe	cta Leu	gtg Val	cta Leu	ctg Leu 80	:	241
ttg Leu	tgg Trp	ata Ile	ctg Leu	aca Thr 85	aca Thr	cca Pro	cat His	gcc Ala	aca Thr 90	atg Met	caa Gln	att Ile	ctg Leu	ctc Leu 95	aca Thr		289
gta Val	aga Arg	ctg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gtg Val	ttt Phe	ctc Leu	aac Asn	ttt Phe 110	ttc Phe	tgt Cys		337
gac Asp	ata Ile	ttt Phe 115	gtt Val	ctc Leu	tta Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asņ		385
gat Asp	ttg Leu 130	atg Met	ata Ile	ctt Leu	atc Ile	atg Met 135	gga Gly	GJA aaa	ctc Leu	atc Ile	att Ile 140	Val	att Ile	cca Pro	ttc Phe		433
ctg Leu 145	Leu	att Ile	gtt Val	ata Ile	tcc Ser 150	Tyr	gca Ala	agg Arg	atc	atc Ile 155	Ser	tct Ser	act Thr	ctt Leu	aag Lys 160		481
gtt Val	cca Pro	tct Ser	act Thr	caa Gln 165	Gly	atc Ile	cac	aag Lys	gto Val	Phe	tct Ser	acc Thr	tgt Cys	ggc Gly 175	tct Ser		529
cat	ctg Leu	tct Ser	gtg Val	. Val	tct Ser	ctg Leu	tto Phe	tat Tyr 185	Gly	aca Thr	att	att :Ile	ggt Gly 190	Leu	tac Tyr		577
tta Leu	tgt Cys	cca Pro 195	Ser	ggt Gly	aat Asn	aat Asn	tto Phe 200	Sei	cta Lev	aag Lys	ggy ggg	Ser 205	Ala	atg Met	gct Ala		625
		туг			gtg Val		Pro						•				649

<210> 377

<211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<400> 377

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Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala 20 25 30

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu 65 70 80

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr 85 90 95

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys 100 105 110

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe 130 135 140

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys 145 150 155 160

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala

195 200 205

Met Met Tyr Thr Val Val Thr Pro 210 215

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<213	> M	us m	uscu	lus	dome	stic	us									
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<221	> m	isc_	feat	ure												
<222			(649													
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			(649										_			
<223	> P	rodu	ct =	olf	acto	ry r	ecep	tor;	reg	ion	betw	een	tran	smem	brane do	mains TM2
and	TM7															
<400		78														40
c tt	c to	t ga	t ct	c tg	c tt	t to	c to	t gt	c ac	a at	g cc	c aa	g tt	g ct	a cag	49
Ph	e Se	r As	p Le	u Cy	rs Ph	ie Se	r Se	er Va			t Pr	о Гл	s Le		u Gln	•
1				5					10	ı				15)	
									_						.0.	0.77
aac	atg	cag	agc	cag	gac	acg	tcc	atc	tcc	tat	gct	ggc	tgt	ctg	aca	97
Asn	Met	Gln		Gln	Asp	Thr	Ser		Ser	TYT	Ala	GТÃ		Leu	Tnr	
			20					25					30			
																145
caa	atg	tac	ttt	tta	ttg	gtt	ttt	gga	gac	ctg	gag	agc	atc	Ctt	Ton	145
Gln	Met		Phe	Leu	Leu	Val		GIY	Asp	Leu	GIU		тте	ьeu	Leu	
		35					40					45				
														a++	ast	193
ttg	gtc	atg	gct	tat	gac	cgg	tat	gtg	get	gcc	cgc	Dha	Dwa	Tou	Uic	193
Leu		Met	Ala	Tyr	Asp	Arg	ıyr	var	ATG	val	60	Pne	PIO	пеп	птэ	
	50					55					60					
									+	~+~		ata	ata	ata	++=	241
tac	atg	agc	atc	atg	agc	CCC	aca mb	Ton	C	y . y	Ora.	Lou	ton	1721	Lou	241
	Met	ser	тте	Met		Pro	THE	ьeu	Cys	75	Cys	Беп	пеп	val	Leu / 80	
65					70					/5					00	
									- + -	++~	a2.a	act	ata	ctc	tta	289
tcc	tgg	gta	דדד	act	gtg	ctg	tat m	Com	wor	LLG	uic	mh~	Lou	Lou	Ley	209
Ser	Trp	vaı	Pne		vaı	Leu	TYL	ser	90	Leu	urs	TIII	пеи	95	neu	
				85					90					93		
					L								+++	++~	tat	337
tct	aga	ttg	tca	TTC	tgt	gag	gat	aac	ttg	alc	tri-	tria	Dho	Dho	Cre	337
Ser	Arg	Leu		Pne	Cys	Glu	Asp		ren	тте	nis	UIS		FIIE	Cys	
			100					105					110			
				_#			المساح مط			*~*	~~~	- + +	6 5+	-++	22t	385
gac	ata	tct	gcc	ctg	CEC	aag	ctg	gct	cgc	Con	gac	att.	ui-	T1-	aaι Nen	363
Asp	He		ATA	ьеи	ьeu	Lys	Leu 120	ATS	cys	ser	ASP	11e	nis	TTG	UDII	
							1.20					143				
		115					120									
					 -	atg			ab+	~++	200		250	cc=	ttc	433

PCT/IB00/02017 WO 01/46262 380 Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe 135 481 tta ctc att gtt gtg tcc tat ata caa att gtc tac tcc att cta aag Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys 155 150 529 att tca tct gct cat gtt tta cac aag atc ttc tcc acc tgt ggg tcc Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser 170 577 cac ctg tct gta gtc tca ctg ttc tat ggg aca att ttt gct ctc tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr 185 180 tta tgt cca tca gct aat aac tct act gtg aag gag att tcc atg gcc 625 Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 200 195 649 atg atg tgc aca gtg gtg act ccc Met Met Cys Thr Val Val Thr Pro 210 215 <210> 379 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963 <400> 379 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 10 Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr 20 Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu 40 35

Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His 50 55 60

Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu 65 70 75 80

Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu

WO 01/46262 381 PCT/IB00/02017

85 90 95

Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 120 125

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe 130 135 140

Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala 195 200 205

Met Met Cys Thr Val Val Thr Pro 210 215

<210> 380

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank =
AF073964

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7

<400> 380

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Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val

1 5 10 15

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cag Gln	att Ile	tat Tyr 35	ttt Phe	ttc Phe	atg Met	ctc Leu	ttt Phe 40	gga Gly	ggc Gly	atg Met	gac Asp	ata Ile 45	ctt Leu	ctc Leu	ctc Leu	145
acc Thr	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	ttt Phe	gtg Val	gcc Ala	atc Ile	tgt Cys 60	cac His	ccc Pro	ctt Leu	cac His	193
tat Tyr 65	tca Ser	gtc Val	att Ile	atg Met	aat Asn 70	ccc Pro	caa Gln	cta Leu	agt Ser	ggc Gly 75	ttg Leu	ctg Leu	gtt Val	ctt Leu	gta Val 80	241
tca Ser	tgg Trp	ttt Phe	att Ile	agc Ser 85	ttt Phe	tca Ser	tat Tyr	tct Ser	ctg Leu 90	ata Ile	cag Gln	agt Ser	cta Leu	ttg Leu 95	atg Met	289
ctg Leu	cgg Arg	ttg Leu	tcc Ser 100	ttc Phe	tgt Cys	aca Thr	aat Asn	cag Gln 105	ata Ile	att Ile	aaa Lys	cac His	ttt Phe 110	tac Tyr	tgt Cys	337
gaa Glu	tat Tyr	tct Ser 115	Arg	gcc Ala	ctc Leu	act Thr	ata Ile 120	gcc Ala	tgc Cys	tca Ser	gac Asp	aca Thr 125	Leu	atc Ile	aat Asn	385
cat His	atc Ile 130	ctt Leu	ctt Leu	tat Tyr	att Ile	ctg Leu 135	ata Ile	tgt Cys	gtc Val	ctt Leu	ggc Gly 140	Phe	atc Ile	cct Pro	ttc Phe	433
tca Ser 145	Gly	ato	ctt Leu	tat Tyr	tca Ser 150	Tyr	tgt Cys	aaa Lys	att Ile	gtt Val 155	Ser	tct Ser	att Ile	ttg Leu	aga Arg 160	481
att Ile	cca Pro	tca Ser	aca Thr	gat Asp 165	Gly	aaa Lys	tat Tyr	aaa Lys	gca Ala 170	Phe	tct Ser	acc Thr	tgt Cys	ggg Gly 175	tct Ser	529
cat	cta Lev	tca Sei	gtg Val	. Val	tct Ser	tta Leu	tto Phe	tate Tyr	Gly	aca Thr	Gly	ctt Lev	ggt Gly 190	Val	tac L Tyr	577
ctt Lei	agt Sei	tci Sei 19	r Ası	gta Val	a act	tcc Ser	Sei 200	c Ser	GJ7	y aag y Lys	gad Asi	gtg Val 205	L Val	g gco	tca Ser	625
gt: Va	a ato 1 Mei 210	Ту	t ac	a gte r Vai	g gto L Val	acc L Thr 215	r Pro	t o								649

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank =

AF073964

<400> 381

Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val 1 5 10 15

Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr 20 25 30

Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu Leu 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val 65 70 75 80

Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
100 105 110

Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn 115 120 125

His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg 145 150 155 160

Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

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180 185 190

Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser 195 200 205

Val Met Tyr Thr Val Val Thr Pro 210 215

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AF0739	965															
<220>																
<221>		1643	,													
	(2)	(643) _1£:	- at o	~, ~	aceni	tor.	rea	ion l	betwe	een 1	trans	smeml	brane o	domains (rm2
<223>		auct =	OIL	acco.	ry r	ecep.	COL,	109								
and T																
<400>	382	gat ct	a ta	~ ++	c tc	a to	c at	c ac	a at	a cc	gaa	a ct	g ct	g aag	49	
gttc	gta	Asp Le	.c cy	e Ph	e Se	r Se	r Va	1 Th	r Va	l Pr	о Ьу	s Le	u Le	u Lys		
	var .	нар ше	:u. Су 5	5 F11	e DC.			10			_		15			
1			,													
	+- a+	a tcg	aca	aac	aaa	acc	atc	tca	ata	gaa	ggc	tgc	ctg	gct	97	
gac c		u Ser	Δla	Lvs	Lvs	Thr	Ile	Ser	Ile	Glu	Gly	Cys	Leu	Ala		
ASP L	eu ne	20	niu	_,,			25					30				
		20					_									
ana a	.tc tt	t ttt	ata	ttt	ttt	cct	tct	ggt	act	gaa	gcc	tgc	ctg	ctc	145	
Cln V	ral Dh	e Phe	Val	Phe	Phe	Pro	Ser	Gly	Thr	Glu	Ala	Cys	Leu	Leu		
GIII	35					40					45					
tet e	tc at	g gct	tat	gac	cgc	tat	gct	gcc	atc	tgc	cat	CCC	ctg	ctc	193	
Ser 1	Jal Me	t Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Ile	Cys	His	Pro	Leu	Leu		
	50		•	_	55					60					•	
															0.44	
tac	aac ca	ag gtg	atg	aga	aat	gag	ttg	tgt	gta	agg	ctt	gtg	gtc	atc	241	
Tvr	Glv G	ln Val	Met	Arg	Asn	Glu	Leu	Cys	Val	Arg	Leu	Val	Val	TIE		
65				70					75					80		
															200	
tca	tag g	gc gtg	gcc	tct	ctc	aac	gca	acc	atc	atc	gtg	ctc	ttg	gct	289	
Ser	Tro G	ly Val	Ala	Ser	Leu	Asn	Ala	Thr	Ile	Ile	Val	Leu	пеи	Ala		
		-	85					90					95			
															227	
atc	aac c	tg gad	ttc	tgt	ggg	gct	caa	acc	att	cac	cac	tac	acc	tgt	337	
Val	Asn L	eu Asp	Phe	Cys	Gly	Ala	Gln	Thr	Ile	His	His	TAT	TILL	cys		
		100					105					110				

	•	V U	1/4020	,,						38	35						
9	gag Glu	ctg Leu	cct Pro 115	gcc Ala	ctt Leu	ttc Phe	ccc Pro	ttg Leu 120	tcc Ser	tgt Cys	tcc Ser	gat Asp	atc Ile 125	tcc Ser	atc Ile	act Thr	385
•	gtc Val	gtc Val 130	gtc Val	ctg Leu	ctt Leu	tgc Cys	tcc Ser 135	agc Ser	ttg Leu	ctg Leu	cat His	ggg Gly 140	ctg Leu	gga Gly	acc Thr	ttt Phe	433
	atc Ile 145	cct Pro	atc Ile	ttc Phe	ttc Phe	tcc Ser 150	tat Tyr	gcc Ala	cgc Arg	att Ile	gtc Val 155	tcc Ser	gcc Ala	atc Ile	ttg Leu	agc Ser 160	481
	atc Ile	agt Ser	tcc Ser	acc Thr	acc Thr 165	GJÀ aaa	agg Arg	agc Ser	aag Lys	gcc Ala 170	ttc Phe	tcc Ser	acc Thr	tgc Cys	tct Ser 175	tcc Ser	529
	cac His	ctc Leu	gct Ala	gca Ala 180	gtg Val	acc Thr	ttg Leu	Phe	ttt Phe 185	ggg	tct Ser	ggc Gly	ttt Phe	ctt Leu 190	tgc Cys	tat Tyr	577
	ctc Leu	atg Met	ccg Pro 195	Pro	tct Ser	ggt Gly	tct Ser	tct Ser 200	ctg Leu	gac Asp	ttg Leu	ctc Leu	ttg Leu 205	tcg Ser	ttg Leu	cag Gln	625
			Ala		acg Thr												643
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	<40	7396 0>	383													Lys	
	Phe 1	e Val	L AS <u>r</u>	o red	5	s Pne	e 'Ser	ser	. va.	10	. val	L		, Dec	15	. 2,2	
	Asr) Let	ı Leı	1 Set 20	r Ala	ı Lys	. Lys	Thi	r Ile 25	e Sei	r Ile	e Glu	ı Gly	7 Cys 30	. Lev	ı Ala	
	Glr	ı Va	1 Ph	e Pho	e Val	l Phe	e Phe	e Pro	o Sei	r Gly	y Th:	r Gli	ı Ala 45	a Cys	s Lei	ı Leu	

Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu

55

50

Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile 65 70 75 80

Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala 85 90 95

Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys 100 105 110

Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr 115 120 125

Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe 130 135 140

Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser 145 150 155 160

Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser 165 170 175

His Leu Ala Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr 180 185 190

Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Ser Leu Gln
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Tyr Ser Ala Val Thr Pro 210

<210> 384

<211> 643

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =

AF073966 <220>

<221> CDS

<222> (2)..(643)

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and T	:м7 - 3	84													,	49	
Leu 1	ı Va	l As	p Il	e Ph 5	e Ph	e Se	r Se	r Va	1 Th 10	r Il	e Pr	o Ly	s Me	t Le 15			
aac o	cat His	ctc Leu	cta Leu 20	ggt Gly	agc Ser	aag Lys	Ala	atc Ile 25	tcc Ser	ttt Phe	Gly	gga Gly	tgt Cys 30	atg Met	gca Ala	97	
cag a	Met	tac Tyr 35	ttc Phe	atg Met	ata Ile	tca Ser	ttg Leu 40	gga Gly	aac Asn	aca Thr	Asp	agt Ser 45	tat Tyr	ata Ile	cta Leu	145	
gct q Ala i	gca Ala 50	atg Met	gca Ala	tat Tyr	gac Asp	cga Arg 55	gct Ala	gtg Val	gct Ala	atc Ile	agt Ser 60	cgc Arg	ccg Pro	ctt Leu	cat His	193	
tat (Tyr)	gca Ala	aca Thr	att Ile	atg Met	agt Ser 70	cca Pro	caa Gln	ctt Leu	tgt Cys	gtc Val 75	ctg Leu	ctg Leu	gtt Val	gct Ala	80 GJA aaa	241	
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gct Ala	aga Arg	ttg Leu	tcc Ser 100	ttc Phe	tgt Cys	ggc Gly	aat Asn	aag Lys 105	gat Asp	gtg Val	gcc Ala	aac Asn	ttc Phe 110	tac Tyr	tgt Cys	337	
gac Asp	att Ile	aca Thr 115	Pro	ttg Leu	ctc Leu	cag Gln	ctg Leu 120	tcc Ser	tgt Cys	tct Ser	gac Asp	atc Ile 125	cgc Arg	ttc Phe	aat Asn	385	
gtg Val	aag Lys 130	Met	atg Met	tac Tyr	ctt Leu	ggg Gly 135	gtg Val	Gly	gtc Val	ttc Phe	tct Ser 140	gtg Val	cca Pro	ctg Leu	ctg Leu	433	
tgc Cys 145	atc Ile	ato Ile	ato Ile	tcc Ser	tat Tyr 150	gtc Val	cgg Arg	gtc Val	ttt Phe	tcc Ser 155	Thr	gtc Val	ttg Leu	cgg Arg	gtt Val 160	481	
cca Pro	tct	acc Thi	aag Lys	ggc Gly 165	Phe	ctg Leu	aag Lys	gcc	ttg Leu 170	Ser	acc Thr	tgt Cys	ggc Gly	Ser 175	cac His	529	
ctg Leu	aca Thr	gto Val	g gtg L Val 180	Ser	ttg Lev	tat Tyr	tat Tyr	ggg Gly 185	Thr	gto Val	atg Met	: Gly	atg Met 190	Тут	ttc Phe	577	
cgg Arg	Pro	cto Let	ı Thi	agt Ser	tac Ty	agt Ser	ctg Lev 200	L Lys	g cat His	gca Ala	a ttg a Lev	ata 1 Ile 209	Thr	gtg Val	g atg Met	625	

PCT/IB00/02017 WO 01/46262 388

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<210> 385

<211> 214

<212> PRT

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =

AF073966

<400> 385

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Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala

Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu 40

Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His 55

Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly 75 65

Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr 85

Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys 105 100

Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn 125 115 120

Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu 140 130

Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val 155 150 145

Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His 170 Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe 185 Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met 200 205 Tyr Thr Ala Val Thr Pro 210 <210> 386 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 386 c ctg gtg gac atc tgc ttt acc act gtc atc gtg cca cag atg tta gtg 49 Leu Val Asp Ile Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val aac ttg ctg aca cag aga aag aca atc ctc ttt gcc cag tgc ctc act 97 Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr 25 20 caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg 145 Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu 35 40 193 gct gcg atg gcc att gac cgc tat gtt gct att tgc aat ccg ctt cat Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His 55 50 tac aac aca gtc atg agt ccc agg cgc tgt cgc ttg ctg gtt gtg gca 241 Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala 70 75

tcc tgg gca gtg tcc cat ctt cac tcc ctc acc cac aca att ctc atg

289

65

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Ser	Trp	Ala	Val	Ser 85	His	Leu	His	Ser	Leu 90		His	Thr	Ile	Leu 95	Met	•
ggt Gly	cgc Arg	ctc Leu	tct Ser 100	ttc Phe	tgt Cys	gga Gly	ccc Pro	aat Asn 105	gtc Val	att Ile	cat His	cac His	ttc Phe 110	ttt Phe	tgt Cys	337
gat Asp	gtc Val	cag Gln 115	cca Pro	ctg Leu	ctg Leu	aca Thr	ctc Leu 120	tcc Ser	tgc Cys	tct Ser	gac Asp	acc Thr 125	tct Ser	atc Ile	aat Asn	385
gag Glu	ctc Leu 130	ttg Leu	gcc Ala	ttc Phe	aca Thr	gag Glu 135	ggc Gly	tct Ser	gtt Val	gta Val	atc Ile 140	atg Met	agc Ser	cct Pro	ttt Phe	433
atc Ile 145	Leu	ttg Leu	ttg Leu	tct Ser	ctt Leu 150	ata Ile	tct Ser	ata Ile	ttc Phe	act Thr 155	cgg Arg	act Thr	gtt Val	ctg Leu	agg Arg 160	481
gtc Val	cct Pro	tca Ser	GJĀ	gaa Glu 165	Gly	agg Arg	tac Tyr	aaa Lys	gtt Val 170	ttc Phe	tct Ser	acc Thr	tgt Cys	ggg Gly 175	Ser	529
cac	ctc Leu	aca Thr	gtt Val 180	Val	gca Ala	ctg Leu	ttc Phe	tat Tyr 185	Gly	acc Thr	ata Ile	ata Ile	tca Ser 190	Val	tac Tyr	577
att Ile	cgc Arg	ccc Pro 195	Ser	tcc Ser	acc Thr	tac Tyr	tca Ser 200	Val	aca Thr	aag Lys	gac	cga Arg 205	Val	gtc	act Thr	. 625
		туг					cca Pro									649
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Gln Met Tyr Phe Phe Val Ala Phe Gly Ile Thr Asp Ser Phe Leu Leu 35 40 45

Ala Ala Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu His

Tyr Asn Thr Val Met Ser Pro Arg Arg Cys Arg Leu Leu Val Val Ala 65 70 75 80

Ser Trp Ala Val Ser His Leu His Ser Leu Thr His Thr Ile Leu Met 85 90 95

Gly Arg Leu Ser Phe Cys Gly Pro Asn Val Ile His His Phe Phe Cys 100 105 110

Asp Val Gln Pro Leu Leu Thr Leu Ser Cys Ser Asp Thr Ser Ile Asn 115 120 125

Glu Leu Leu Ala Phe Thr Glu Gly Ser Val Val Ile Met Ser Pro Phe 130 135 140

Ile Leu Leu Leu Ser Leu Ile Ser Ile Phe Thr Arg Thr Val Leu Arg 145 5 50 150 50 160

Val Pro Ser Gly Glu Gly Arg Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Thr Ile Ile Ser Val Tyr 180 185 190

Ile Arg Pro Ser Ser Thr Tyr Ser Val Thr Lys Asp Arg Val Val Thr 195 200 205

Val Ile Tyr Thr Val Val Thr Pro 210 215

<210> 388

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<212> DNA

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1				5					10							
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caa Gln	Met	tac Tyr 35	ttt Phe	ttc Phe	agt Ser	Val	ttt Phe 40	gga Gly	agt Ser	ctg Leu	gag Glu	ata Ile 45	ttc Phe	ctt Leu	ctt Leu	145
gta Val	gtc Val 50	ctg Leu	gcc Ala	tat Tyr	gac Asp	cgc Arg 55	tat Tyr	gtg Val	gcc Ala	atc Ile	tgt Cys 60	tta Leu	ccc Pro	ctt Leu	caa Gln	193
tat Tyr 65	tcc Ser	agc Ser	atc Ile	atg Met	agc Ser 70	ccc Pro	aat Asn	ctc Leu	tgt Cys	gtg Val 75	tgt Cys	gtg Val	gtg Val	gtg Val	ttc Phe 80	241
tgc Cys	tgg Trp	gta Val	ttt Phe	att Ile 85	gtg Val	ttt Phe	tat Tyr	gcc Ala	atg Met 90	ttt Phe	cac His	aca Thr	cta Leu	ctc Leu 95	ttg Leu	289
gct Ala	aga Arg	ttg Leu	tca Ser 100	ttt Phe	tgt Cys	aag Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	cca Pro	cac His	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	ata Ile	tct Ser 115	gcc Ala	ctt Leu	ctg Leu	aag Lys	ttg Leu 120	gca Ala	tgc Cys	tct Ser	gat Asp	gtt Val 125	tat Tyr	att Ile	aat Asn	385
gaa Glu	tta Leu 130	atg Met	ata Ile	ctt Leu	atc Ile	ttg Leu 135	gga Gly	GJA aaa	ttt Phe	ctt Leu	ctt Leu 140	gtc Val	atc Ile	tca Ser	ctc Leu	433
tta Leu 145	Leu	atc Ile	att Ile	gta Val	tcc Ser 150	Tyr	gta Val	caa Gln	att Ile	gtc Val 155	Ser	tca Ser	att Ile	tta Leu	agg Arg 160	481
att Ile	tct Ser	tct Ser	act Thr	cgg Arg 165	Ala	atc Ile	cat His	aag Lys	ctc Leu 170	Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tca Ser	529
cac His	ctg Leu	tct Ser	gtg Val	gtc Val	tca Ser	ctg Leu	ttc Phe	tat Tyr	. Gla gaa	aca Thr	att	att Ile	ggt Gly	ctg Leu	tac Tyr	577

180 185 190

tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc 625 Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser

195 200 205

ctg atg tac aca gtg gtg act ccc
Leu Met Tyr Thr Val Val Thr Pro
210 215

<210> 389

<211> 216

<212> PRT

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968

<400> 389

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Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140 394

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 155 Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 170 . 165 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 Leu Met Tyr Thr Val Val Thr Pro 215 . <210> 390 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR1M; Accession DDBJ/EMBL/GenBank = AF073969 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 390 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca 97 Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 25 caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt 145 Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40 193 gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55 tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta 241 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu

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65 _.					70					7 5					80		
ttg Leu	tgg Trp	atg Met	cta Leu	aca Thr 85	aca Thr	tcc Ser	cat His	gcc Ala	atg Met 90	atg Met	cat His	act Thr	ctc Leu	ctt Leu 95	gca Ala	. 2	89
gca Ala	aga Arg	ttg Leu	tct Ser 100	ttt Phe	tgt Cys	gag Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ctc Leu	aat Asn	ttt Phe 110	ttc Phe	tgt Cys	3	37
gac Asp	cta Leu	ttt Phe 115	gtt Val	ctc Leu	cta Leu	aag Lys	ctg Leu 120	gct Ala	tgc Cys	tca Ser	gac Asp	act Thr 125	tat Tyr	gtt Val	aat Asn	3	85
			ata Ile													4	133
ttc Phe 145	ctc Leu	att Ile	gtc Val	atg Met	tct Ser 150	tat Tyr	gca Ala	agg Arg	atc Ile	att Ile 155	gcc Ala	tcc Ser	att Ile	ctt Leu	aag Lys 160	4	181
gtt Val	cca Pro	tct Ser	att Ile	caa Gln 165	ggg	atc Ile	tac Tyr	aag Lys	gtc Val 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggt Gly 175	tcc Ser	5	529
cat His	ctg Leu	tct Ser	gtg Val 180	Val	acc Thr	ttg Leu	ttt Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggt Gly 190	ctc Leu	tac Tyr		577
tta Leu	tgt Cys	cca Pro 195	Ser	ggt Gly	aat Asn	aat Asn	tcc Ser 200	aca Thr	gta Val	aag Lys	Gly	act Thr 205	Val	atg Met	gcc Ala	(625
		Tyr	aca Thr				Pro						•			1	6 4 9
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Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 35 40

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75 80

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 100 105 110

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120 125

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 130 135 140

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 145 150 155 160

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205

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aat			aca Thr 20	aag					acc	tat				att	tct	97	
			ttt Phe													145	
			gcc Ala													193	
			atc Ile													241	
			aca Thr													289	
_		_	tcc Ser 100		_		-									337	
			caa Gln													385	
_	_		atg Met													433	
			ctt Leu								Ser				_	481	
			tca Ser		Gly					Ser						529	
cac	ctc	tca	gtt	gtt	tca	tta	ttc	tat	tct	aca	ctc	ttg	ggt	gcg	tat	577	

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr 180 185 190

ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca tct
Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser

195 200 205

gtt atg tac agt gtg gtc acc ccc

Val Met Tyr Ser Val Val Thr Pro

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Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val 1 5 10 15

Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser 20 25 30

Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His 50 55 60

Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly 65 70 75 80

Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys
100 105 110

Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn 115 120 125

Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu 130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala 145 150 155 160
Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser 165 170 175
His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr 180 185 190
Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser 195 200 205
Val Met Tyr Ser Val Val Thr Pro 210 215
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caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt 145 Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45
gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60
tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu 65 70 75 80

tcc Ser	tgg Trp	gtg Val	ctg Leu	acc Thr 85	act Thr	ttc Phe	cat His	gcc Ala	atg Met 90	ctg Leu	cat His	acc Thr	ctg Leu	ctc Leu 95	atg Met		289
gcc Ala	aga Arg	ttg Leu	tca Ser 100	ttc Phe	tgt Cys	gag Glu	gac Asp	aat Asn 105	gtg Val	atc Ilė	ccc Pro	tac Tyr	ttt Phe 110	ttc Phe	tgt Cys		337
gac Asp	atg Met	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	tcc Ser	tgc Cys	tct Ser	gac Asp	act Thr 125	cac His	gtt Val	aat Asn		385
gaa Glu	ttg Leu 130	gtg Val	ata Ile	ttt Phe	gtc Val	aca Thr 135	gga Gly	ggc	ctg Leu	atc Ile	ctt Leu 140	gtc Val	att Ile	cca Pro	ttt Phe		433
gtg Val 145	ctc Leu	atc Ile	ctt Leu	gtg Val	tcc Ser 150	tat Tyr	gca Ala	cga Arg	att Ile	gtg Val 155	tcc Ser	tcc Ser	att Ile	ctc Leu	aag Lys 160		481
gtc Val	ccg Pro	tct Ser	gct Ala	cga Arg 165	ggc	atc Ile	cgt Arg	aaa Lys	gcc Ala 170	Phe	tcc Ser	acc Thr	tgt Cys	ggg Gly 175	tcc Ser		529
cac His	ctg Leu	tct Ser	gtg Val 180	Va1	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	atc Ile	att Ile	ggt Gly 190	ctg Leu	tac Tyr		577
tta Leu	tgt Cys	cca Pro 195	Ser	gct Ala	gat Asp	aac Asn	tct Ser 200	Thr	gtg Val	aag Lys	gaa Glu	act Thr 205	Val	atg Met	gcc Ala		625
		Туг			gtg Val		Pro										649
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<40 Phe 1)0> e Sei	395 (As)	o Let	1 Cys 5	s Phe	e Sei	s Sei	c Vai	1 Th:	r Mei	e Pro	Ly:	s Le	1 Let 15	ı Gln		

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr 20 25 30

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu 35

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu 65 70 80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys 100 105 110 110 110 110 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn 115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe 130 135 140

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala 195 200 205

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aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 25 30
Caa atg tac ttc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu 35 40 45
gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60
tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 70 75 80
tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289 Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu 85 90 95
act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt 337 Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110
gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125
gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt 433 Glu Leu Met Ile Met Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130 135 140
cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa 481 Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 145 150 155 160
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg tct Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175
cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac 577 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 180 185 190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct 625 Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200 195 649 atg atg tac act gtg gtg att ccc Met Met Tyr Thr Val Val Ile Pro <210> 397 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972 Phe Thr Asp Leu Cys' Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 10 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 20 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu 40 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55 Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 75 70 65 Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu 85 Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 · 105 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn

125

115 120

130

135

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe

404 Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 150 Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170 His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 185 180 Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200 Met Met Tyr Thr Val Val Ile Pro 210 <210> 398 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 398 c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln 10 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala 25 20 caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu 40 35 gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat 193 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His 50 55 241 tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu 80 70 75 65

tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta

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Ser	Trp	Ala	Leu	Thr 85	Thr	Leu	Tyr	Ala	Met 90	Leu	His	Thr	Leu	Leu 95	Leu	
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	aaa Lys	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gac Asp	ctt Leu	tct Ser 115	gct Ala	ctc Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
gag Glu	tta Leu 130	atg Met	ata Ile	atg Met	ata Ile	att Ile 135	gga Gly	gca Ala	ctt Leu	gtt Val	gtt Val 140	ata Ile	ctt Leu	cca Pro	ttt Phe	433
cta Leu 145	Leu	atc Ile	ata Ile	gtg Val	tct Ser 150	tat Tyr	gcg Ala	cac His	att Ile	gtc Val 155	Ser	tcc Ser	act Thr	ctc Leu	aaa Lys 160	481
gtc Val	cct Pro	tca Ser	act Thr	cga Arg 165	Gly	atc Ile	cac His	aag Lys	gtc Val 170	Phe	tcc Ser	act Thr	tgt Cys	ggt Gly 175	tct	529
cat	ctg Leu	tct Ser	gtg Val	. Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	tca Ser	gto Val	att	gtt Val 190	. Leu	tac Tyr	577
tta Lev	tgt Cys	cca Pro	Ser	tct Ser	aat Asn	aac Asn	tct Ser 200	Thi	gtg Val	g aag L Lys	gat Asp	act Thr 205	· Val	atg L Met	tct Ser	625
atg Met	g ato : Met 210	ту	e act	gtg Val	gtg Val	act Thr 215	Pro	:								649
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Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu 35

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His 50 55 60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu 65 70 75 80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu 85 90 95

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Cys 100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 130 135 140

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys 145 150 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 195

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<222> (1)..(649)

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1 cac i	rtc -	ctc :	ato (5 gag a	aaa a	aag a	acc a	atc	10 tct	ttt	gcc	cta	tgt :	15 ggg	acc	97	
His 1	Phe :		Met (20	Glu 1	Lys 1	Lys '		Ile 25	Ser	Phe .	Ala :	Leu	30 CAS	GTĂ .	Thr		
cag (Gln)	Leu	ttc Phe 35	ttt Phe	gct Ala	ctg Leu	Thr	ctt Leu 40	Gly	gga Gly	act Thr	Glu	ttt Phe 45	ctg Leu	ttg Leu	ctg Leu	145	
act .	gcc Ala 50	atg Met	gcc Ala	tat Tyr	Asp	cgc Arg 55	tat Tyr	gtg Val	gct Ala	gtc Val	tgt Cys 60	aat Asn	cca Pro	tta Leu	cgg Arg	193	
tac Tyr 65	aca Thr	gtg Val	gtg Val	atg Met	aac Asn 70	cca Pro	agg Arg	ctc Leu	tgc Cys	atg Met 75	ggt Gly	cta Leu	gca Ala	ggt Gly	gtc [~] Val 80	241	
tct Ser	tgg Trp	ttt Phe	gtg Val	ggt Gly 85	gta Val	gtt Val	aat Asn	tct Ser	gct Ala 90	gtg Val	gag Glu	aca Thr	gca Ala	gtc Val 95	acc Thr	289	
atg Met	tac Tyr	ctt Leu	ccc Pro 100	acc Thr	tgt Cys	Gly ggg	cac His	aat Asn 105	gta Val	ctc Leu	aac Asn	cat His	gtg Val 110	gcc Ala	tgt Cys	337	
gag Glu	aca Thr	ctg Leu 115	gca Ala	ctg Leu	gtc Val	aga Arg	ctg Leu 120	gcc Ala	tgt Cys	gtg Val	gac Asp	atc Ile 125	acc Thr	ctc Leu	aac Asn	385	
caa Gln	gtg Val 130	Val	ata Ile	ctg Leu	gct Ala	tct Ser 135	agt Ser	gtg Val	gtg Val	gtg Val	ctg Leu 140	atg Met	ata Ile	ccc Pro	tgc Cys	433	
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Ile	Arg	Ser	acc Thr	Gln 165	Gly	Arg	Arg	Lys	170	Phe	: Glu	Thr	· Cys	Ala 175	Ser	529	
cat His	ctg	r act	gtg Val	. Val	tcc Ser	atg Met	tct Ser	tat Tyr 185	Gly	, atg , Met	gcc : Ala	cto Lev	tto Phe 190	Thr	tac Tyr	577	
ctg	cag	g cct	gcc	tcc	aca	gcc	tct	gct	gag	gcag	g gac	aag	gtg	gta	gtg	625	

-

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 195 200 205

atc ttc tat gct ttg gtc acc ccc
Ile Phe Tyr Ala Leu Val Thr Pro
210 215

649

<210> 401

<211> 216

<212> PRT <213> Mus musculus domesticus

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<222> (1)..(649)

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His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr 20 25 30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu Leu 35 40 45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg 50 55 60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val 65 70 75 80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr 85 90 95

Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys 100 105 110

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn 115 120 125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys 130 135 140

Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys 145 150 155 160 Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser 165 His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr 185 Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 200 195 Ile Phe Tyr Ala Leu Val Thr Pro <210> 402 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 402 t ttc gtt gac ctc tgc cag tcc agt gtc atc atg ccc aaa atg ctg gag 49 Phe Val Asp Leu Cys Gln Ser Ser Val Ile Met Pro Lys Met Leu Glu aaa ttt gtc atg gtg aag agt gtc att tct ttt gca gaa tgc atg gct 97 Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala 20 145 cag tit tac tia tit gat git tit gct git tea gag tgt cac atg ctg Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 45 35 40 get gtc atg get tat gat ege tat gtt gec ate tgt aac eec ttg eta 193 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu 50 55 241 tat aat gtt acc atg tct tac aaa gtg tgt tcc tgg atg gta gtg ggg Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 80 70 65 289 gtg tat agt gta ggc ttg att tgt gcc aca ggg gaa aca gtc tgc ctg

Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu

85

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ctt a	aga Arg	ctg Leu	cta Leu 100	ttc Phe	tgc Cys	aaa Lys	Ala	gat Asp 105	gac Asp	ata Ile	aac Asn	cac His	tac Tyr 110	ttc Phe	tgt Cys	337
gat (Asp	ctt Leu	tta Leu 115	cca Pro	cta Leu	ctg Leu	gaa Glu	caa Gln 120	tcc Ser	tgt Cys	tcc Ser	aat Asn	aca Thr 125	ttt Phe	atc Ile	aat Asn	385
gaa Glu	ata Ile 130	cta Leu	gga Gly	ctg Leu	tcc Ser	ttc Phe 135	agt Ser	tca Ser	ttt Phe	aat Asn	act Thr 140	act Thr	gtc Val	cca Pro	gct Ala	433
ctg Leu 145	acc Thr	atc Ile	ctc Leu	agt Ser	tcc Ser 150	Tyr	atc Ile	ttc Phe	atc Ile	ata Ile 155	gcc Ala	agc Ser	atc Ile	ctc Leu	cgc Arg 160	481
att Ile	cct Pro	tcc Ser	act Thr	gaa Glu 165	Gly	agg Arg	tcc Ser	aaa Lys	gcc Ala 170	Phe	agc Ser	acc	tgc Cys	agc Ser 175	ser	529
cac His	atc Ile	ttg Leu	gct Ala 180	Val	gct Ala	gtc Val	ttc Phe	ttt Phe 185	Gly	tct Ser	tta Leu	gca Ala	ttc Phe 190	met	tac Tyr	577
ctt Leu	cag Gln	cca Pro	Ser	tca Ser	gto Val	ago Ser	Ser 200	Met	gac : Asp	caa Glr	Gly ggg	aaa Lys 205	val	tco Ser	tct Ser	625
gtg Val	ttt Phe 210	ту	acc Thr	att	gti Va:	gtg l Val	Pro	; >		•				,		649
<21 <21 <21	1> 2>	403 216 PRT	<21	3> 1	Mus	musci	ılus	dom	esti	cus						
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<40 Phe 1	iu> e Va	403 1 As	p Le	u Cy . 5	s Gl	n Se	r Se	r Va	1 Il 10	e Me	t Pr	o Ly	s Me	t Le 15	u Glu	
Lys	s Ph	e Va	1 Me 20		l Ly	s Se	r Va	1 I1 25	e Se	r Ph	e Al	a Gl	u Cy 30	s Me	t Ala	

Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu 45 40 35

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu

55

Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly 70

Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu 85

Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys 105 100

Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn . 120

Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala 130 135 140

Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg 155 150 145

Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser . 170 165

His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr 185 180

Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser . 205 195 200

Val Phe Tyr Thr Ile Val Val Pro 215 210

<210> 404

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

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<221> CDS

<222> (2)..(649)

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Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gin 1 15												
aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca 97 Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20 25 30												
caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 35 40 45												
gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60												
tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu 70 80												
tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta 289 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 85 90 95												
act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt 337 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110												
gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 115 120 125												
gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 130 135 140												
cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 145 150 155 160												
gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct 529 Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175												
cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac 577 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190												
tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct 625 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195 200 205												

649 ctg atg tac act gtg gta act ccc Leu Met Tyr Thr Val Val Thr Pro 215 210 <210> 405 <211> 216 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976 <400> 405 Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 5. Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 25 20 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 40 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 60 50 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 70 75 65 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu 85 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120 115 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 135 130

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys

150

145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195

Leu Met Tyr Thr Val Val Thr Pro 210 215

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<211> 650	
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<221> CDS ·	
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<pre><222> Product = olfactory receptor; region between transmembrane</pre>	COMMITTED TITE
and TM7	
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cc ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg	
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu 10 15	
1 5 10 15	
cag aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg	95
Gln Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu	
20 25 30	
20 23	
aca caa atg tac tit tic agt gtt tit gga agt ctg gag ata tic ctt	143
Thr Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu	
35 40 45	
33	
ctt gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt	191
Leu Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu	
50 55 60	
50	
caa tat tee age ate atg age eee aat ete tgt gtg tgt gtg gtg	239
Gln Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val	
65 70 75	
05	
ttc tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc	287
Phe Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu	
Phe Cys Trp Val Phe 11e Val Phe Tyr Ald Met Phe HIS IM 200 200	

ttg gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc 335

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Leu Ala Arg Leu	Ser Phe Cys 100	Lys Asn	Asn Val Il 105	e Pro His Phe 110	Phe
tgt gac ata tct g Cys Asp Ile Ser 1 115	gcc ctt ctg Ala Leu Leu	aag ttg Lys Leu 120	gca tgc tc Ala Cys Se	et gat gtt tat er Asp Val Tyr 125	att 383 Ile
aat gaa tta atg Asn Glu Leu Met 130	ata ctt atc Ile Leu Ile	ttg gga Leu Gly 135	ggg ttt ct Gly Phe Le	et ctt gtc acc eu Leu Val Thr 140	tca 431 Ser
ctc tta ctc atc Leu Leu Leu Ile 145	att gta tcc Ile Val Ser 150	tat gta Tyr Val	caa att gt Gln Ile Va 15	al Ser Ser Ile	tta 479 Leu
agg att tct tct Arg Ile Ser Ser 160	act cgg gct Thr Arg Ala 165	atc cat Ile His	aag ctc tt Lys Leu Ph 170	cc tcc acc tgt ne Ser Thr Cys	ggc 527 Gly 175
tca cac ctg tct Ser His Leu Ser	gtg gtc tca Val Val Ser 180	ctg ttc Leu Phe	tat ggg gg Tyr Gly Al 185	ca att att ggt la Ile Ile Gly 190	ctg 575 Leu
tac tta tgt cca Tyr Leu Cys Pro 195	tca gct aat Ser Ala Asn	aac tct Asn Ser 200	act gaa aa Thr Glu Ly	ag gag act gcc ys Glu Thr Ala 205	atg 623 Met
tcc ctg atg tac Ser Leu Met Tyr 210					650
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Asn Met Gln Ile 20	Gln Asp Thi	r Pro Ile 25	e Ser Tyr V	al Ala Cys Leo 30	1 Thr
Gln Met Tyr Phe 35	Phe Ser Va	l Phe Gly 40	y Ser Leu G	Glu Ile Phe Le 45	ı Leu
Val Val Leu Ala 50	Tyr Asp Ar	g Tyr Val		Cys Leu Pro Le	ı Gln

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Thr Ser Leu 130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

<210> 408

<211> 648

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

741												
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aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr 20 25 30	97											
caa atg tac ttt ttc agt gtt ttt ggg agt ctg gag ata ttc ctt ctt Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45	145											
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60	193											
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg ttc Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Phe 65 70 75 80	241											
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu 85 90 95	289											
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110	337											
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125	385											
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140	433											
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg 145 150 155 160	481											
att tot tot act ogg got atc cat aag otc tto too acc tgt ggo toa Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175	529 577											
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 190	625											
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 195 200 205	648											
ctg atg tac aca gtg gtg act cc	040											

Leu Met Tyr Thr Val Val Thr 210 215

<210> 409

<211> 215

<212> PRT <213> Mus musculus domesticus

:220>

<221> misc_feature

<222> (1)..(648)

<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<400> 409

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Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu 130 135 140

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 185 180 Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser 200 Leu Met Tyr Thr Val Val Thr 210 <210> 410 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank = AF073979 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 410 c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag 49 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca 97 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr 25 20 caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt 145 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu 35 gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat 193 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55 50 tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc 241 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu

65

70

85

100

tet tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu

gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys

90

110

289

gac Asp	ata Ile	tct Ser	gcc Ala	ctg Leu	ctc Leu	aag Lys	ttg Leu 120	gcc Ala	tgc Cys	tct Ser	gac Asp	att Ile 125	tct Ser	att Ile	aat Asn	385
gaa Glu	cta Leu 130	atg Met	ata Ile	ttt Phe	atc Ile	gtg Val 135	gga Gly	GJA aaa	ctt Leu	gat Asp	act Thr 140	gta Val	atc Ile	cca Pro	ttt Phe	433
tta Leu 145	ctc Leu	att Ile	gtt Val	gtt Val	tcc Ser 150	tat Tyr	gta Val	caa Gln	att Ile	gtc Val 155	tgc Cys	tcc Ser	att Ile	cta Leu	aag Lys 160	481
ttc Phe	tca Ser	tct Ser	aca Thr	cgg Arg 165	ggc Gly	ata Ile	cac His	aag Lys	gtc Val 170	ttc Phe	tcc Ser	acc Thr	tgt Cys	ggc Gly 175	tcc Ser	529
cac His	ctg Leu	tct Ser	gtg Val 180	gtc Val	tca Ser	ctg Leu	ttc Phe	tat Tyr 185	Gly	aca Thr	att Ile	att Ile	ggt Gly 190	gtc Val	tac Tyr	577
ata Ile	tgc Cys	cca Pro 195	tca Ser	gct Ala	aat Asn	aac Asn	tct Ser 200	act Thr	gtg Val	aag Lys	gag Glu	act Thr 205	gtc Val	atg Met	tcc Ser	625
ctg Leu	atg Met 210	Tyr	aca Thr	gtg Val	gtg Val	acg Thr 215	ccc Pro		•				•			649
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			_fea .(64		:											•
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Asr	ı Met	: Glr	1 Sei 20	Glr	n Asp	Pro	Se:	25	e Pro	тул	Ala	a Ser	Cys 30	: Le	1 Thr	
Glr	n Mei	t Ту: 35	r Ph	e Phe	e Me	t Ala	a Pho 40	e Gly	y As	n Met	E Gl	u Ile 45	э Туг	c Le	ı Leu	
Va.	l Va 50	l Me	t Al	а Ту	r As	p Arg 55	д Ту	r Va	l Al	a Il	e Cy 60		e Pro	o Le	u His	

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu 65 70 75 80

Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn 115 120 125

Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe 130 135 140

Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys 145 150 155 160

Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr 180 185 190

Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

<210> 412

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

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<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2
and TM7

<400> 412

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aac Asn	atg Met	caġ Gln	agc Ser 20	caa Gln	gtt (Val	cct Pro	tca Ser	atc Ile 25	ccc Pro	tat Tyr	gca Ala	Gly	tgc Cys 30	ctg Leu	aca Thr	97
caa Gln	atg Met	tac Tyr 35	ttc Phe	ttt Phe	ttg Leu	Phe	ttt Phe 40	gga Gly	gat Asp	ctt Leu	gag Glu	agc Ser 45	ttc Phe	ctc Leu	ctt Leu	145
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	tat Tyr	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193
tac Tyr 65	acc Thr	agc Ser	att Ile	atg Met	agc Ser 70	ccc Pro	agg Arg	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctt Leu	gtg Val	ctg Leu	ctg Leu 80	241
tcc Ser	tgg Trp	ttg Leu	ctg Leu	acc Thr 85	atg Met	tcc Ser	cat His	tcc Ser	atg Met 90	ctg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337
gat Asp	ctg Leu	tct Ser 115	Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385
Glu	Leu 130	Val	Ile	Leu	atc Ile	Ile 135	Gly	Gly	Leu	Val	Val 140	Ile	Leu	Pro	Phe	433
Leu 145	Leu i	Val	Thr	Val	Pro 150	Tyr	Ala	. Arg	Ile	11e 155	Ser	Ser	Ile	Leu	160	481
Val	Pro	Ser	Thr	165	Gly	Ile	His	: Lys	Val 170	. Phe	: Ser	Thr	Cys	Gly 175		, 529
His	s Leu	ı Sei	7 Val	. Val	. Ser	Leu	Phe	185	Gly	7 Thr	: Ile	e Ile	: Gly 190	Leu	tac Tyr	577
tt: Le:	a tgt u Cys	cca Pro 19	Ser	gct -Ala	aat Asn	aac Asn	tct Sei 200	Thi	cta Lei	a aag	g gad s Asp	act Thr 205	· Val	atg Met	tct Ser	625
		t Ty			g gta l Val		. Pro									649

<210> 413

<211> 216

<212> PRT <213> Mus musculus domesticus

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

<400> 413

Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 10

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 20

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu 40

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His . 50

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 70 75

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 90

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 100 105

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120 115

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 135 130

Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 150 145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170 165

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 185 185

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 195 200 205

Leu Met Tyr Thr Val Val Thr Pro 210 215

<210> 414													
11> 649													
<212> DNA <213> Mus musculus domesticus													
<220>													
<221> misc_feature													
<pre><222> (1)(649) <223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981</pre>													
<220>													
<221> CDS													
<222> (2)(649)	2												
<pre><222> (2)(042) <223> Product = olfactory receptor; region between transmembrane domains TM</pre>													
and TM7													
<400> 414 c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49													
Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln													
- 10 IS													
1 5 10 13													
aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97													
Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala													
20 25 30													
caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agc tta ctc ctt 145													
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu													
35 40 45													
33													
gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat 193													
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His													
50 55 60													
tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241													
Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu													
65 70 75 80													
tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289													
Ser Tro Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu													
85 90 95													
227													
act agg ttg tet tte tgt aaa aac aat gtg ate eee cat ttt tte tgt 337													
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys													
100 105 110													
385													
gac ctt tot got oto otg aag otg goo tgo tot gat att cac att aat 385													

WO 01/46262		425	PCT/IB00/02017
Asp Leu Ser Ala Leu 115	Leu Lys Leu A 120	la Cys Ser Asp Ile His 125	Ile Asn
gag tta atg ata atg Glu Leu Met Ile Met 130	g ata att gga go : Ile Ile Gly A 135	ca ctt gtt gtt ata ctt la Leu Val Val Ile Leu 140	cca ttt 433 Pro Phe
cta ctc atc ata gtg Leu Leu Ile Ile Val 145	g tot tat gog c L Ser Tyr Ala H 150	ac att gtc tcc tcc att is Ile Val Ser Ser Ile 155	ctc aaa 481 Leu Lys 160
gtc cct tca act cga Val Pro Ser Thr Arg 16	g Gly Ile His L	ag gtc ttc tcc act tgt ys Val Phe Ser Thr Cys 170	ggt tct 529 Gly Ser 175
cat ctg tct gcg gt His Leu Ser Ala Va 180	l Ser Leu Phe T	at ggg tca gtc att gtt Tyr Gly Ser Val Ile Val 185 190	. Leu Tyr
tta tgt cca tca tc Leu Cys Pro Ser Se 195	t aat aac tct a r Asn Asn Ser T 200	act gtg aag gat act gto Thr Val Lys Asp Thr Val 205	atg tct 625 Met Ser
atg atg tac act gt Met Met Tyr Thr Va 210 '	g gtg act ccc l Val Thr Pro 215		649
<220> <221> misc_featur <222> (1)(649)		omesticus 7M; Accession DDBJ/EMB	L/GenBank = AF073981
		Val Thr Met Pro Asn Ph 10	
Asn Met Gln Ser G		Ile Pro Tyr Ala Gly Cy 25 30	s Leu Ala
Gln Met Tyr Phe P 35	he Leu Phe Phe 40	Gly Asp Val Glu Ser Le	ou Leu Leu

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 50 55 60

WO 01/46262	426	PCT/IB00/02017

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu 90 85 .

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys 105 100

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120 115

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe 135 130

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys 155 150 145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170 165

His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr 190 185 180

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser 200 205

Met Met Tyr Thr Val Val Thr Pro 210

<210> 416

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 416

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag 49 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln

WO 01/46262		427	PCT/IB00/02017	
1	5	10	15	
aat ata cag agc c Asn Ile Gln Ser G 20	ag gac cca tcc ln Asp Pro Ser	atc ccc tat gca Ile Pro Tyr Ala 25	ggc tgc ctg gca 97 Gly Cys Leu Ala 30	
caa aca tac ttc t Gln Thr Tyr Phe F 35	tt atg gtt ttt he Met Val Phe 40	gga ġat atg gag Gly Asp Met Glu	agc ttc ctt ctt 145 Ser Phe Leu Leu 45	
gtg gcc atg gcc t Val Ala Met Ala I 50	at gac cgc tat Yr Asp Arg Tyr 55	gtg gcc atc tgc Val Ala Ile Cys 60	ttc cct ctg cat 193 Phe Pro Leu His	
tac acc agc atc a Tyr Thr Ser Ile 1 65	atg agt ccc aaa Met Ser Pro Lys 70	ctc tgt ggt tgt Leu Cys Gly Cys 75	cta atg ctg cta 241 Leu Met Leu Leu 80	
Leu Trp Met Leu !	aca aca tcc cat Thr Thr Ser His 35	gcc atg atg cat Ala Met Met His 90	act ctc ctt gca 289 Thr Leu Leu Ala 95	
gca aga ttg tct Ala Arg Leu Ser 100	ttt tgt gag aac Phe Cys Glu Asn	aat gtg atc ctc Asn Val Ile Leu 105	aat ttt ttc tgt 337 Asn Phe Phe Cys 110	
gac cta ttt gta Asp Leu Phe Val 115	ctc cta aag ctg Leu Leu Lys Leu 120	Ala Cys Ser Asp	c act tat gtt aat 385 p Thr Tyr Val Asn 125	
gag ttg atg ata Glu Leu Met Ile 130	ttt ata atg agt Phe Ile Met Sex 135	tcc ctc ctc att Ser Leu Leu Ile 140	t gtt att cca ttt 433 e Val Ile Pro Phe 0	
ttc ctc att gtc Phe Leu Ile Val 145	atg tct tat gca Met Ser Tyr Ala 150	a agg atc att gco a Arg Ile Ile Ala 155	c tcc att ctt aag 481 a Ser Ile Leu Lys 160	
gtt cca tct att Val Pro Ser Ile	caa ggg atc tad Gln Gly Ile Tyn 165	c aag gtc ttc tc c Lys Val Phe Se: 170	c acc tgt ggt tcc 529 r Thr Cys Gly Ser 175	
cat ctg tct gtg His Leu Ser Val 180	gtg acc ttg tt Val Thr Leu Ph	t tat ggg aca at e Tyr Gly Thr Il 185	t att ggt ctc tac 577 e Ile Gly Leu Tyr 190	
tta tgt cca tca Leu Cys Pro Ser 195	ggt aat aat tc Gly Asn Asn Se 20	r Thr Val Lys Gl	gg act gtc atg gcc 625 Ly Thr Val Met Ala 205	
atg atg tac aca Met Met Tyr Thr 210	gcg gtg act cc Ala Val Thr Pr 215	c o	6 49	

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<210> 417 <211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982

<400> 417

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 5 10

Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala 25 20

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu 40 35

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 60 50 55

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu 65 70 75

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala 85 90

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys 105

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn 115 120

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe 135 140 130

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys 150

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser 170

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr

180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala 195 200 205

Met Met Tyr Thr Ala Val Thr Pro 210 215

<210>	41	8														
<211>	64	9							_							
<212>	DNA <213> Mus musculus domesticus															
<220>																
<221>	<221> misc_feature															
<222> (1)(649)																
<pre><223> Taxon = 10092; clone = OR912-47M4; Accession DDBJ/EMBL/GenBank =</pre>																
AF073983																
<220>																•
<221>	CD	S														
<222>	(2	:)((649))										1		domains TM2
<223>	Pr	oduc	:t =	olfa	actor	ry re	ecept	or;	reg:	ion i	petwe	een	crans	smenu	orane	domains TM2
and TM																
<400>	41	18												- at	~ ~t=	49
c ttt	gtg	gad	ato	c tg	t tti	t acc	c tc	c ac	c ac	t gt	C CC	a aa	g ats	g CL	y yta	#J
Phe	Va3	L Ası	, Ile	е Су	s Pho	e Th	r Se:	r Th	r Th	r va	I Pr	о гъ	s me	15	u Val	
1				5					10					13		
												~~~	tat:	a++ :	adc	97
aat a	ta d	cag a	act (	caa	agc	aag (	gcc	acc .	aca mb	cat '	yca Na	yac Nen	Cve	Tle	Ser	
Asn I	le (			Gln	Ser	Lys .	ATA .	TTE.	THE	TYL .	ALG	veħ	30	116	501	
			20					25					50			
								~~~	~~~	++~	aac	220	ttt	ctc	cta	145
cag a	tg	tct	gtc	ttc -1	ttg	gtt	Dha	yca xis	Clu	T.OU	Acn	Agn	Phe	Leu	Leu	
Gln M			Val	Pne	гел	vaı	40	Ala	GIU	пеа	r.op	45				
		35					40									
gct g					~~~	aa2	+=+	ata	act	atc	tat	cac	cca	tta	tat	193
gct g Ala V	tg	atg	31-	mm	yac Aen	Ara	Tyr	Val	Ala	Ile	Cvs	His	Pro	Leu	Tyr	
		Met	Ald	TĀT	rsp	55	-3-				60					
5	0					J_										
tac a		~+ ~	-++	att	aac	саа	cat	ctc	tat	ata	ctg	atg	gtt	ctg	ctg	241
Tyr T	iCa ib~	y.c.	Tla	wal	Agn	Gln	His	Leu	Cvs	Ile	Leu	Met	Val	Leu	Leu	
65	111	Val	110	V CL	70				_	75					80	
65																
tcc t	-~~	att	att	agg	atc	cta	cat	gcc	ttc	tta	cag	agc	tca	att	gtg	289
Ser 1	מאנו	Wal	Val	Ser	Ile	Leu	His	Ala	Phe	Leu	Gln	Ser	Ser	Ile	Val	
Ser .	LIP	•		85					90					95		
cta	720	tta	acc	ttt	tat	gga	gat	gta	aaa	att	ccc	cac	ttc	ttc	tgt	337
Leu (-ay -ln	Len	Thr	Phe	Cvs	Glv	Asp	Val	Lys	Ile	Pro	His	Phe	Phe	Cys	
neu (يات لا	100		-1-		_	105	_				110			
gag	att	220	cac	cha	tet	caa	ctc	aca	tgt	tca	gac	agc	ttt	tca	agc	385
gag '		عسد	cug	0.09					-							

V O 01/40202		4	30		
Glu Leu Asn Gln 115	Leu Ser Gln	Leu Thr Cys	Ser Asp Ser 125	Phe Ser	Ser
caa ctc ata atg Gln Leu Ile Met 130	aat ctt gta Asn Leu Val 135	cct gtt cta Pro Val Leu	ttg gca gtc Leu Ala Val 140	att tcc Ile Ser	ttc 433 Phe
agt agt atc ctt Ser Ser Ile Leu 145	tac tct tat Tyr Ser Tyr 150	ttc aag ata Phe Lys Ile	gtg tcc tcc Val Ser Ser 155	ata tgt Ile Cys	tct 481 Ser 160
atc tcc tca gtt Ile Ser Ser Val	caa ggg aag Gln Gly Lys 165	tac aag gca Tyr Lys Ala 170	a Phe Ser Thr	tgt gtc Cys Val 175	tct 529 Ser
cac ctt tcc att His Leu Ser Ile 180	gtc tcc tta Val Ser Leu	ttt tat ag Phe Tyr Se 185	t aca ggc ctt r Thr Gly Leu	gga gtg Gly Val 190	tat 577 Tyr
gtc agt tct gtt Val Ser Ser Val 195	gtg atc caa Val Ile Glr	agc tct ca Ser Ser Hi 200	c tcț gct gca s Ser Ala Ala 205	Arg Ala	tct 625 Ser
gtg atg tat act Val Met Tyr Thr 210	gtg gtc acc Val Val Thi 21	Pro			649
<210> 419 <211> 216 <212> PRT <213 <220> <221> misc_fea	3> Mus musc ature	ulus domesti	.cus		
AF073983	19) 10092; clon	e = OR912-47	M4; Accessio	n DDBJ/EI	MBL/GenBank =
<400> 419 Phe Val Asp Ile 1	e Cys Phe Th 5	r Ser Thr Ti	nr Val Pro Ly)	s Met Le 15	u Val
Asn Ile Gln Th		rs Ala Ile T 25	hr Tyr Ala As	p Cys Il 30	e Ser
Gln Met Ser Va 35	l Phe Leu Va	al Phe Ala G 40	lu Leu Asp As 45	n Phe Le	u Leu

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 50

Tyr Thr Val Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

80 75 70 65

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 90 85

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys 105 100

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Phe Ser Ser 120

Gln Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe 140 135

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 150 155

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 175 170

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 185 180

Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser 200 195

Val Met Tyr Thr Val Val Thr Pro 215 210

<210> 420

<211> 646

<212> DNA <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank = AF073984

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 420

c tot gtg gat gta tgc ttc tcc tcc acc act gtc cct aag gta ctg gcc 49

									434							
Se 1	r Va	l As	p Va	1 Cy 5	s Pho	e Sei	: Se	r Thi	10	r Vai	l Pro	o Lys	s Val	15	u Ala	
att Ile	cac His	Ile	cta Leu 20	aga Arg	aat Asn	caa (Gln i	Ala	att t Ile : 25	cg Ser	ttc Phe	tct (Ser (GIY (tgc (Cys : 30	ctc Leu	aca Thr	97
cag Gln	ctg Leu	tat Tyr 35	ttt Phe	ctc Leu	tgt Cys	gtg Val	ttt Phe 40	gct (gac Asp	atg Met	Asp .	aat Asn 45	ttc Phe	ctg Leu	ctg Leu	145
gct Ala	gtg Val 50	atg Met	gcc Ala	tat Tyr	gac Asp	cga Arg 55	ttt Phe	gtg Val	gcc Ala	ata Ile	tgc Cys 60	cac His	cct Pro	tta Leu	cac His	193
Туг 65	Thr	Thr	Lys	Met	Thr 70	cat His	Gln	Leu	Cys	75	Pne	гел	Val	vai	80	241
Ser	Trp	Met	Val	Ala 85	Ser	ctg Leu	Asn	Ala	90	ьeu	urs		nea	95	Val	289
gct Ala	caa Gln	ctc Leu	tac Tyr 100	Phe	tgt Cys	GJÀ ããa	gac Asp	aat Asn 105	gtg Val	atc Ile	ccc Pro	cac His	ttc Phe 110	ttc Phe	tgt Cys	337
Glu	ı Val	Thr 115	Pro	Leu	Leu	aaa Lys	Leu 120	Ser	Cys	Ser	Asp	125	HIS	neu	ASII	385
Glı	130	ı Met	: Ile	e Leu	ı Ala	135	Ala	CTA	ren	TIE	140	ьец	AIA	FIC	ttt Phe	433
Va:	1 Cy: 5	s Ile	e Lei	ı Let	1 Ser 150	Tyr)	· Ile	e Leu	Ile	155	Cys	S Ala	116	. Dec	aaa Lys 160	481
at Il	c tc e Se	a tc	c aca	a gga r Gly 16	y Arg	a tgg g Trp	aaa Lys	a gcc s Ala	tto Phe 170	e ser	aco Thr	c tgt Cys	: ggc	Sei 17!	a cac r His	529
tt Le	g gc u Al	t gt a Va	t gt 1 Va 18	l Cy	c cto s Le	c tto u Phe	e tai	t ggd r Gly 189	/ Th	t ate	c ata e Ile	a too e Sei	c cto Lev 190	ı ıy.	t ttc r Phe	577
aa As	c cc n Pr	c to o Se 19	r Se	t tc r Se	t ca r Hi	c tc: s Se:	a gc r Al 20	a Gl	g ag y Ar	g ga g As	c ato p Me	g gca t Ala 20	a Al	t gc a Al	c atg a Met	625
at Me	ig ta et Ty 21	r Th	a gt ir Va	g gt il Va	g ac	c cc r Pr 21	0									646

<210> 421 <211> 215 <212> PRT <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(646) <223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank = AF073984 <400> 421 Ser Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala 10 5 Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr 25 20 Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu 40 35 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His 60 55 50 Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly 70 65 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val 90 85 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys 100 . 105 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn 115 Glu Leu Met Ile Leu Ala Val Ala Gly Leu Ile Met Leu Ala Pro Phe

135

165

Val Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ala Cys Ala Ile Leu Lys

Ile Ser Ser Thr Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His

130

145

140

Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ser Leu Tyr Phe 180 185 Asn Pro Ser Ser Ser His Ser Ala Gly Arg Asp Met Ala Ala Met 200 Met Tyr Thr Val Val Thr Pro 210 <210> 422 <211> 650 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(650) <223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/ GenBank = AF073985 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 422 c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag atg ctg gta 49 Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc 97 Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser cag atg tct gtc ttc ttg gtt ttt gga gaa ctg gac aac ttt ctc ctg 145 Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn Phe Leu Leu gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat 193 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 55 tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg 241 Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gta

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val

cta cag ttg acc ttt tgt gga gat gta aga att ccc cac ttc ttc tgt Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys 289

WO 01/46262	435	PCT/IB00/02017

. WO 01/46262	435						
100	105	110					
gag ctt aac cag ctg tct Glu Leu Asn Gln Leu Ser 115	caa ctc aca tgt tca gac a Gln Leu Thr Cys Ser Asp S 120	gc tta tca agc 385 er Leu Ser Ser 25					
cac ctc ata atg cat ct His Leu Ile Met His Leu 130	gta cct gtt cta ttg gga g 1 Val Pro Val Leu Leu Gly A 135 140	rcc att tcc ttc 433 la Ile Ser Phe					
agt agt atc ctt tac tc Ser Ser Ile Leu Tyr Se 145	t tat ttc aag ata gtg tcc t r Tyr Phe Lys Ile Val Ser 8 0 155	cc ata tgt tct 481 Ger Ile Cys Ser 160					
atc tcc tca gtt caa gg Ile Ser Ser Val Gln Gl 165	g aag tac aag gca ttt tct a y Lys Tyr Lys Ala Phe Ser 5 170	aca tgt gtc tct 529 Thr Cys Val Ser 175					
cac ctt tcc att gta tc His Leu Ser Ile Val Se 180	c tta ttt tat agt aca ggc o r Leu Phe Tyr Ser Thr Gly 1 185	ctt gga gtg tat 577 Leu Gly Val Tyr 190					
gtc agt tct gct gtg gt Val Ser Ser Ala Val Va 195	c caa agc tct cac tct gct al Gln Ser Ser His Ser Ala 200	gca aga gcc tct 625 Ala Arg Ala Ser 205					
gtg atg tat act gtg gt Val Met Tyr Thr Val Va 210	cc aca cac g al Thr His 215	650					
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Asn Ile Gln Thr Gln S	Ser Lys Ala Ile Thr Tyr Ala 25	Asp Cys Ile Ser 30					
Gln Met Ser Val Phe 1 35	Seu Val Phe Gly Glu Leu Asp 40	Asn Phe Leu Leu 45					
Ala Val Met Ala Tyr : 50	Asp Arg Tyr Val Ala Ile Cys 55 60	B His Pro Leu Tyr					

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu 75 65 70

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 90 85

Leu Gln Leu Thr Phe Cys Gly Asp Val Arg Ile Pro His Phe Phe Cys 105 100

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp Ser Leu Ser Ser 120 115

His Leu Ile Met His Leu Val Pro Val Leu Leu Gly Ala Ile Ser Phe 135 130

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 155 150 145

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 170 165

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 185 180

Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser 205 200 195

Val Met Tyr Thr Val Val Thr His 210

<210> 424

<212> DNA <213> Mus musculus domesticus

<220>

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR912-47M8; Accession DDBJ/EMBL/GenBank =

AF073986

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<221> CDS

<222> (2)..(649)

437	
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<pre><400> 424 c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag gtg ctg gta Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Val Leu Val 1 5 10 15</pre>	49
aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser 20 25 30	97
cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctc ctg Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu 35 40 45	145
gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 50 55 60	193
tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu 65 70 75 80	241
tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gtg Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 85 90 95	289
cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgc Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys 100 105 110	337
gag ctt aac cag ctg tct caa ctc aca tgt tta gac agc ttt tca agc Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser 115 120 125	385
cac ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe 130 135 140	433
agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 145 150 155 160	481
atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 165 170 175	529
cac ctt tcc att gtc ttc tta ttt tat agt aca ggc ctt gga gtg tat His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 180 185 190	577
gtc agt tct gct gtg gtc caa agc tct cac tct gct gca aga gcc tct Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser 195 200 205	625

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gtg atg tat act gtg gtc acc ccg Val Met Tyr Thr Val Val Thr Pro 210

649

<210> 425 <211> 216

<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR912-47M8; Accession DDBJ/EMBL/GenBank = AF073986

<400> 425

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Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser 20 25 30

Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr 55

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu 70 75

Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val 90

Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys 105

Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser 120 115

His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe 140 135 130

Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser 155 150 145

Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser 170 165 His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr 185 180 Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser 205 200 195 Val Met Tyr Thr Val Val Thr Pro 210 <210> 426 <211> 649 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(649) <223> Taxon = 10092; clone = OR912-47M9; Accession DDBJ/EMBL/GenBank = AF073987 <220> <221> CDS <222> (2)..(649) <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7 <400> 426 49 c ttt gca gat ctc tgc ttt tct act acc aca gtg ccc cag gtg ctt gtc Phe Ala Asp Leu Cys Phe Ser Thr Thr Thr Val Pro Gln Val Leu Val 10 cac ttc ctg gtg aag agg aag acc att tct ttt gct gga tgt tct aca 97 His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr 25 20 cag ata gtg gtg ttg ctt ctg gtc gga tgc aca gag tgt gca ctg ctg 145 Gln Ile Val Val Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu 40 35 gca gtg atg tcc tat gac cga tat gtg gct gtc tgc aaa cct ctg cac 193 Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His 50 tac tcc acc atc atg aca cac tgg cta tgt gtt cag ctg gct gca ggg 241 Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly 75 70 65 tcc tgg gcc agt ggt gca ctt gtg tcc ctg gtg gat acc aca ttc aca 289 Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr

90

85

95

		·		
tta cgt ctt cct t Leu Arg Leu Pro 1	tat cga gga aad Tyr Arg Gly Ası	c aat gtc att n Asn Val Ile 105	aac cac ttt ttc Asn His Phe Phe 110	tgt 337 Cys
gaa cct cct gcc o Glu Pro Pro Ala I 115	ctc ctg aag ct Leu Leu Lys Le 12	u Ala Ser Ala	gat aca tac agc Asp Thr Tyr Ser 125	aca 385 Thr
gag atg gcg atc g Glu Met Ala Ile 1 130	ttt gca atg gg Phe Ala Met Gl 135	t gtg gta atc y Val Val Ile	ctc cta gca cct Leu Leu Ala Pro 140	gtc 433 Val
tcc ctc atc ctc Ser Leu Ile Leu 145	acc tcc tac tg Thr Ser Tyr Tr 150	gg aac atc atc p Asn Ile Ile 155	tcc act gta atc Ser Thr Val Ile	cag 481 Gln 160
atg cag tct ggg Met Gln Ser Gly	gaa gga agg ct Glu Gly Arg Le 165	tc aag gtc tto eu Lys Val Phe 170	tcc acc tgt ggc Ser Thr Cys Gly 175	tcc 529 Ser
cac ctc att gtt His Leu Ile Val 180	gtt gtt ctc tt Val Val Leu Ph	to tac ggc to he Tyr Gly Ser 185	a gca ata ttt gcc Ala Ile Phe Ala 190	tac 577 Tyr
atg agg ccc aac Met Arg Pro Asn 195	Ser Lys Ile Me	tg aat gaa aa et Asn Glu Ly 00	g gat aaa atg att s Asp Lys Met Ile 205	tcg 625 Ser
gtg ttc tat tca Val Phe Tyr Ser 210	gca gtg acc co Ala Val Thr P 215	cg ro		649
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His Phe Leu Val 20		Thr Ile Ser Pl 25	he Ala Gly Cys Se 30	r Thr

Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu 35

Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His 55 50

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly 75 70

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr 90 85

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys 100 105

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr 125 115 120

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val 135

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln 145 . 150

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser 165 170

His Leu Ile Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr 185 180

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser 200 195

Val Phe Tyr Ser Ala Val Thr Pro 215 210

<210> 428

<211> 649

<212> DNA <213> Mus musculus domesticus

<220>

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<222> (1)..(649)

<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<220>

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and	> Pi TM7	codu	st =	olfa												domains	TM2
c tt Ph 1	c act	r Asj	p Leu	1 Cys 5	s Phe	e Ser	Ser	· Val	10	r Me	t Pro	o rA:	з ьес	15	g cag ı Gln		
aac Asn	atg (Gln	agc (Ser (20	caa g Gln V	gtt d Val I	ect tero s	er 1	tc d le 1 25	ecc Pro	tat : Tyr .	gca g Ala (GTA (tgc (Cys 1 30	ctg (Leu '	aca Thr	97	
caa Gln	Met	tac Tyr 35	ttc Phe	ttt i	ttg 1 Leu 1	Phe 1	tt g Phe (gga g Bly i	gat Asp	ctt Leu	GIU	agc Ser 45	ttc (Phe :	ctc Leu	ctt Leu	145	í
gtg Val	gcc Ala 50	atg Met	gcc Ala	tat : Tyr .	Asp :	cga † Arg † 55	tat (Tyr '	gta Val	gcc Ala	atc Ile	tgc Cys 60	ttc Phe	cct Pro	ctt Leu	cat His	193	
tac Tyr 65	acc Thr	agc Ser	att Ile	Met	agc Ser 70	ccc Pro .	agg Arg	ctc Leu	tgt Cys	gtg Val 75	agt Ser	ctt Leu	gtg Val	ctg Leu	ctg Leu 80	241	
tcc	tgg Trp	ttg Leu	ctg Leu	acc Thr 85	atg Met	tcc Ser	cat His	tcc Ser	atg Met 90	ctg Leu	cac His	act Thr	ttg Leu	ctc Leu 95	tta Leu	289	
act Thr	agg Arg	ttg Leu	tct Ser 100	ttc Phe	tgt Cys	gaa Glu	aac Asn	aat Asn 105	gtg Val	atc Ile	ccc Pro	cat His	ttt Phe 110	ttc Phe	tgt Cys	337	
gat Asp	ctg Leu	tct Ser 115	gct Ala	ctg Leu	ctg Leu	aag Lys	ctg Leu 120	gcc Ala	tgc Cys	tct Ser	gat Asp	att Ile 125	cac His	att Ile	aat Asn	385	
gaa Glu	ttg Leu 130	Val	ata Ile	ttg Leu	atc Ile	ata Ile 135	gga Gly	Gly	ctt Leu	gtt Val	gtt Val 140	TIE	ctt Leu	cca Pro	ttt Phe	433	
cta Lei 14:	ı Lev	gtc Val	aca Thr	gtg Val	tct Ser 150	Tyr	gca Ala	cgc Arg	ato Ile	ato Ile 155	ser	tcc Ser	att Ile	ctc	aag Lys 160	481	
gte Va	e cct 1 Pro	tca Sei	a act	cga Arg 165	Gly	atc Ile	cac His	aag Lys	gto Val 170	l Phe	tco Ser	act Thr	tgt Cys	ggt Gly 175	tct Ser	529	
са Ні	c ctq s Len	j tci ı Se:	t gtg r Val	l Val	, tca L Ser	ctg Leu	ttc Phe	tat Tyr 185	G1;	g aca y Thi	a att	att E Ile	ggc Gly	пес	tac 1 Tyr	577	•
tt Le	a tg u Cy	t cc s Pr	a tct o Sei	t gct r Ala	aat Asr	aac Asi	tct Ser	act Thi	ct Le	a aa u Ly	g gad s Asj	c act	t gto	ate L Me	g tct t Ser	625	5

649

200

205 195

ctg atg tac act gtg gta act ccc Leu Met Tyr Thr Val Val Thr Pro 215 210

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<212> PRT <213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<400> 429

Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln 10 5

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr 30 25

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His 55

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu 75 70

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu 90

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys 105 100

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn 120 115

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe 140 135 130

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys 155 150 145

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser 170 165 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr 180 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser 205 200 195 Leu Met Tyr Thr Val Val Thr Pro 210 <210> 430 <211> 1865 <212> DNA <213> Mus musculus domesticus <220> <221> misc_feature <222> (1)..(1865) <223> Taxon = 10090; clone = OR1-72M13; cell line = NIH3T3; Accession DDBJ/EMBL/GenBank = AF073989 <220> <221> CDS <222> (547)..(1482) <223> Product = olfactory receptor; orthologous to human gene OR1-72 <400> 430 ctgcagagtg agttctagga cagccaggac tacacagaga aaccctgaat caaaataaaa 60 taaaataaaa tacaatagaa taaaataaaa taaacaaaaa agaaaaaaga agataaagat gtctaagaga agaatgagat ttcaaaagga atggatacag agaaggtatg gtcatattca 180 cagagacett tetgaatgat cagaacttag tgtaaccact gaaaaatgtt gagaagtgaa 240 gttggaaatc agagttgatc catcataaag gattacagca cttttagaaa ctgactgctt 300 tgatctaaca cttccagagg ttatctggtc ttcatgtggt ttaaaatttg tagagttagc agttctaagt agagataagg tagagaaact aataatgatg agaaaatgca ggattcctaa 420 tttttattgt aataaaagct ttatgtacag ttattccaac acataaaagg acagagacct tagagactgt agtgtatgtt cctcaatctt tctctccagt aggtgtctag cttatttgtc 540 aacaac atg aaa cca gaa aac caa aca aaa tat ttt aga att ttt gct 588 Met Lys Pro Glu Asn Gln Thr Lys Tyr Phe Arg Ile Phe Ala

tct ggg gtt ttc caa tat cca gag cat caa ccc atg cta ttt gga ctg

Ser Gly Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu

636

WO 01/46262 .	··	445	PCT/IB00/02017
15	20	25	30
ttt ctg ctc atg ttt open the Leu Leu Met Phe 35	Val Val Ala Val L	ett ggg aat ctt ctc atc eu Gly Asn Leu Leu Ile 0 45	att 684 Ile
ctg gcc gtc agc att Leu Ala Val Ser Ile 50	gac tct cac ctg c Asp Ser His Leu H 55	eat act ccc atg tac ttc His Thr Pro Met Tyr Phe 60	ttt 732 Phe
cta tct aac ctg tcc Leu Ser Asn Leu Ser 65	ttt tct gac att g Phe Ser Asp Ile 6 70	ggt ttc atc tct aca act Gly Phe Ile Ser Thr Thr 75	gtc 780 Val
cct aag atg ttg gtg Pro Lys Met Leu Val 80	aat atc caa aca c Asn Ile Gln Thr C 85	cag agc aag tcc atc tcc Gln Ser Lys Ser Ile Ser 90	tat 828 Tyr
gca gaa tgc atc acc Ala Glu Cys Ile Thr 95	cag att tat ttt t Gln Ile Tyr Phe 1	ttc atg ctc ttt gga ggc Phe Met Leu Phe Gly Gly 105	atg 876 Met 110
gac aca ctt ctc ctc Asp Thr Leu Leu Leu 115	Thr Val Met Ala	tat gac cga ttt gtg gcc Tyr Asp Arg Phe Val Ala 120 125	. TIE
tgt cac cca ctt cac Cys His Pro Leu His 130	tat tca gtc att Tyr Ser Val Ile 135	atg aat cct caa cta agt Met Asn Pro Gln Leu Ser 140	ggt 972 Gly
ttg cta gtt ctt gta Leu Leu Val Leu Val 145	tca tgg ttt att Ser Trp Phe Ile 150	agc ttt tca tat tct ctg Ser Phe Ser Tyr Ser Let 155	g ata 1020 1 Ile
cag agt cta ttg atg Gln Ser Leu Leu Met 160	g ctg cgg ttg tcc t Leu Arg Leu Ser 165	ttc tgt aca aat cag ata Phe Cys Thr Asn Gln Ile 170	a att 1068 e Ile
aaa cac ttt tac tgt Lys His Phe Tyr Cys 175	t gaa tat gcc aaa s Glu Tyr Ala Lys 180	gcc ctc act ata gcc tg Ala Leu Thr Ile Ala Cy 185	c tca 1116 s Ser 190
gat aca cta atc aas Asp Thr Leu Ile Ass 19	n His Ile Leu Leu	tat att gtg ata tgg gt Tyr Ile Val Ile Trp Va 200 20	T Dea
ggc ttc atc cct tt Gly Phe Ile Pro Ph 210	c tca ggg atc ctt e Ser Gly Ile Leu 215	tat toa tac tat aaa at Tyr Ser Tyr Tyr Lys Il 220	t ttt 1212 e Phe
tct tca att ttg ag Ser Ser Ile Leu Ar 225	ga att cca tca aca ng Ile Pro Ser Thr 230	a gat gga aaa tat aaa go Asp Gly Lys Tyr Lys Al 235	ca ttt 1260 La Phe

WO 01/46262 446	
tct acc tgt ggg tct cat cta tcg gtg gtt tct tta ttc tat ggg aca Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr 240 245 250	.308
ggc ctt agt gtg tac ctt agt tct gat gct act tcc tcc tct ggg aag Gly Leu Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys 255 260 265 270	L356
ggc gtg gtg gcc tca gta atg tat aca gtg gtc acc ccc atg ctg aac Gly Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn 275 280 285	1404
cct ttc atc tac agc ttg agg aac aaa gac att aag aag gcc tta aaa Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys 290 295 300	1452
aca ctt ggg aga ata ctt ctt tta aag tga taatttcact ggttttagac Thr Leu Gly Arg Ile Leu Leu Leu Lys 305 310	1502
atctgaactg atagaaataa aatagtgaac taaagaaatt ctgtactata atcatgtaga	1562
aattttatcc agtttgttgg tctatctttg attaaaatta tactgtgaat atttctatct	1622
gaaatttcta tgatgcctcc ttttttattc gaagttcttt gtctcctccc ctgttttata	1682
cgacatattt ctttacttca gtacaaagtc tacatttcag catgccaata taaccattca	1742
aataccaatt catgaattgt ttagtaaaag ttatgcaatg gctcatttac agaaagtcca	1802
tgtatatata tataacactg ttgtgggttg gtccgactct gtattctgat attaattctg	1862
cag	1865
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<pre><400> 431 Met Lys Pro Glu Asn Gln Thr Lys Tyr Phe Arg Ile Phe Ala Ser Gly 1 5 10 15</pre>	
The Tou	

Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu Phe Leu 20 25 30

Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile Leu Ala 35

Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser 50 55 60

Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val Pro Lys 65 70 80

Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu 85 90 95

Cys Ile Thr Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Thr 100 105 110

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His 115 120 120 125

Pro Leu His Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu 130 135 140

Val Leu Val Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser 145 150 155 160

Leu Leu Met Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His 165

Phe Tyr Cys Glu Tyr Ala Lys Ala Leu Thr Ile Ala Cys Ser Asp Thr 180 185 190

Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe 195 200 205

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser 210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr 225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu 245 250 250

. Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys Gly Val 260 265 270

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys Thr Leu 290 295 300

Gly Arg Ile Leu Leu Leu Lys 305 310